

# YOUNG CONAWAY STARGATT & TAYLOR, LLP

MELANIE K. SHARP  
DIRECT DIAL: (302) 571-6681  
DIRECT FAX: (302) 576-3333  
msharp@ycst.com

THE BRANDYWINE BUILDING  
1000 WEST STREET, 17TH FLOOR  
WILMINGTON, DELAWARE 19801  
  
P.O. BOX 391  
WILMINGTON, DELAWARE 19899-0391

(302) 571-6600  
(302) 571-1253 FAX  
(800) 253-2234 (DE ONLY)  
www.youngconaway.com

December 5, 2007

## **BY E-FILE**

The Honorable Mary Pat Thyng  
United States District Court of Delaware  
844 North King Street  
Wilmington, DE 19801

Re: *Human Genome Sciences, Inc. v. Amgen, Inc. et al.*  
C. A. No.: 07-526 (\*\*\*)  
Letter Brief Regarding Issues on Appeal

Dear Judge Thyng:

Defendants Amgen and Immunex ("Immunex") file this letter brief identifying the issues on appeal to assist the Court in determining the scope of discovery in this action under 35 U.S.C. § 146 ("146 action"). After an extensive evidentiary record was developed during the substantive motion phase of the interference on appeal, the Board of Patent Appeals and Interferences ("Board") found the Human Genome Sciences ("HGS") claims involved in the interference unpatentable under 35 U.S.C. § 102(e) ("§ 102(e)") and that Immunex was the Senior Party. Because the Senior Party is presumed to be the first to invent the subject matter of the interference and HGS had no patentable claims involved in the interference, the Board terminated the interference without reaching the priority phase and consequently without considering the issue of priority.

In this 146 action, which "is essentially a proceeding to review the action of the Board." *Boston Scientific Scimed, Inc. v. Medtronic Vascular, Inc.*, 497 F.3d 1293, 1298 (Fed.Cir. 2007), the Court's review is limited to the Board's decisions in the substantive motion phase of the interference. Because the priority phase of the interference was never reached, the issue of priority was not addressed by the Board and is therefore not on appeal. Moreover, even with respect to those issues decided by the Board, the scope of the appeal of the Board's decision is limited to the legal theories presented below. Discovery must be limited to those legal theories. Examination of those legal theories reveals that no discovery from Immunex is warranted because the legal theories on appeal are limited to either HGS' own information or the objective disclosure of an Immunex or HGS patent reference.

## **I. BACKGROUND**

This action is an appeal of the Board's decision in Interference No. 105,381 ("the '381 Interference") between Junior Party Ni *et al.* and Senior Party Rauch *et al.* The real party in interest for Ni *et al.* is HGS. The real party in interest for Rauch *et al.* is Immunex, a wholly owned subsidiary of Amgen. An interference is an *inter partes* administrative proceeding to determine which party first invented the subject matter of the interference as defined by the interference "count." 37 C.F.R. § 41.201. The claims designated as corresponding to the count ("involved claims") are the claims at risk in the interference whereby the prevailing party may be

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

entitled to a patent on its claims and the losing party is not. A three-member administrative patent judge panel from the Board's Interference Division Trial Section, which exclusively hears patent interferences, issued the decision now on appeal.

An interference is divided into two phases, a substantive motion phase and a priority phase, each lasting about 8 months. Order-Preliminary Motion Times (Ex. A attached hereto); Order-Priority Times (Ex. B attached hereto). During the substantive motion phase the parties may file various motions including motions for judgment (*e.g.*, patentability based on enablement, written description, etc.) which, if granted, may terminate the interference in the movant's favor. Upon completion of the substantive motion phase there may be a separate and distinct priority phase during which the parties submit motions and evidence to show they were first to invent the subject matter of the interference. Typically, first to invent evidence involves inventor and corroborating witness testimony and notebook and other documentation reflecting acts of conception, actual reduction to practice, and diligence. In either phase a party may request discovery upon a showing that the discovery is "in the interests of justice." 37 C.F.R. § 41.150(c).

In this case, Count 1, the sole count in the interference, was directed to a tumor necrosis factor receptor (TNFR) family polypeptide called TRAIL Receptor-2 or TR-2. Decision-Motions (hereinafter "D-M"), Ex. C attached hereto, at 3:22-4:4. In the decision on the substantive motions, the Board granted Immunex's motion for judgment that all of HGS' patent claims involved in the interference were unpatentable under § 102(e) in view of Immunex's U.S. Patent No. 6,072,047 ("the '047 Patent"). D-M, Ex. C at 38:2-5; 74:12-16. The Board also found that Immunex and HGS were entitled to the filing dates of certain earlier filed patent applications for the benefit of priority as to Count 1. D-M, Ex. C at 73:20-23; 74:6-9. In short, the Board found that Immunex remained the Senior Party, which is the party presumed to have invented the count first. Because HGS had no patentable claims in the interference and Immunex was Senior Party, the Board ordered HGS to show cause why judgment should not be entered against it. Decision-Order to Show Cause (hereinafter "D-O"), Ex. D attached hereto at 3:6-9. The Board found HGS' response insufficient and entered judgment adverse to HGS on July 27, 2007, three weeks after the priority phase was initiated and seven months before the priority phase was set to end. D-O, Ex. D at 12:5-6. The Board also found that HGS' priority record had been improperly submitted and ordered it expunged. Order-Expunging Paper (hereinafter "O-EP"), Ex. E attached hereto at 3:6-9. This 146 action is an appeal of the substantive motion phase of the '381 Interference.

## II. ARGUMENT

In this 146 action, the priority phase is not on appeal. The Board's decision to grant Immunex's motion for judgment under § 102(e), to accord Immunex Senior Party status, and to terminate the interference without considering the issue of priority are the case dispositive issues on appeal. The Court cannot consider issues not raised before the Board and should not address issues not decided by the Board. Discovery should be limited accordingly.

### A. THE STANDARD OF REVIEW IN A 146 ACTION

Because a 146 action is a review of an administrative proceeding, the standard of review is governed by the Administrative Procedures Act. *Dickinson v. Zurko*, 527 U.S. 150, 152 (1999). A court reviews "Board decisions pursuant to the permissive rules governing patent interference proceedings for abuse of discretion" and accepts the Board's interpretation of Patent

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

and Trademark Office regulations unless that interpretation is "plainly erroneous or inconsistent with the regulation." *Eli Lilly Co. v. Bd. of Regents of the Univ. of Wash.*, 334 F.3d 1264, 1266 (Fed.Cir. 2003). The Board's decisions of law are reviewed *de novo*. *In re Gartside*, 203 F.3d 1305, 1316 (Fed.Cir. 2000). Unless new evidence or live testimony is permitted on an issue during a 146 action, factual determinations of the Board are reviewed for substantial evidence. *Cell Genesys, Inc. v. Applied Research Sys.*, 499 F.Supp.2d 59, 71 (D.Mass. 2007) ("If the district court does not receive any new evidence, or perhaps any live testimony, it applies the substantial evidence test.").<sup>1</sup> If, however, a district court, under its discretion allows the presentation of evidence or live testimony not available to the Board, factual findings on those issues for which the new evidence or testimony is allowed are made *de novo*. *Winner Int'l Royalty Corp. v. Wang*, 202 F.3d 1340, 1347 (Fed.Cir. 2000) ("the admission of live testimony on all matters before the Board in a section 146 action ... makes a factfinder of the district court and requires a *de novo* trial."); *Genentech, Inc. v. Chiron Corp.*, 220 F.3d 1345, 1351 (Fed.Cir. 2000) (where the district court did not hear live testimony on all issues decided by the Board, "[u]nder *Winner*, live testimony on the issue of practical utility makes the district court a factfinder on that issue, and requires the court to decide that issue *de novo*").

**B. ONLY ISSUES DECIDED BY OR RAISED BEFORE THE BOARD ARE ON APPEAL IN A 146 ACTION**

An issue may not be appealed under § 146 unless the issue was decided by the Board or raised by the parties during the proceedings below. *Conservolite, Inc. v. Widmayer*, 21 F.3d 1098, 1100 (Fed.Cir. 1994) ("The issues presented by the parties were not raised during the interference; therefore, they were not properly before the district court."). A 146 action "is not a chance for a party to reconstruct its case, based on a new litigation strategy, leapfrogging the administrative process in the PTO." *Conservolite*, 21 F.3d at 1102. It "is primarily intended to provide an opportunity for further, live testimony by witnesses who presented affidavits or depositions to the Board, which may not receive live testimony, so that the credibility of those witnesses can be better judged." *Cell Genesys*, 499 F.Supp.2d at 61. In *Conservolite*, the district court awarded priority based on an issue not raised in the interference proceeding. Neither party objected to the district court's consideration of the new issue and both parties briefed the merits of the issue on appeal to the Federal Circuit. *Sua sponte*, the Federal Circuit reversed the district court, holding "the court's decision and admission of testimony on this [new] issue was an abuse of discretion." *Conservolite*, 21 F.3d at 1103.

In *dicta*, the Federal Circuit has suggested that "the district court may, in appropriate circumstances, exercise its discretion and admit testimony on issues even though the issues were not raised before the Board." *General Instrument Corp. v. Scientific-Atlanta, Inc.*, 995 F.2d 209, 214 (Fed.Cir. 1993) ("fraud relating to the interference proceeding itself may be one such issue"). See also *Conservolite*, 21 F.3d at 1103 ("right to raise such issues is limited to *compelling* circumstances" (emphasis added)).

The *Conservolite* majority soundly rejected the notion that because a 146 action may involve *de novo* review, issues not raised before the Board may be considered. During the November 21, 2007 telephonic conference with the Court, HGS cited what it represented was the

<sup>1</sup> *Cell Genesys* is a recent and thorough analysis of case law regarding 146 actions. This case has been certified for interlocutory appeal to the U.S. Court of Appeals for the Federal Circuit pursuant to 28 U.S.C. § 1292(b). Federal Circuit Case No. 08-M865.

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

"concurrence" in *Conservolite* for the proposition that "in a proceeding under 146, the parties can create a new record, present new evidence ... highlighting the fact that this is a trial *de novo*...." Transcript, Ex. F attached hereto at 12:18-22. In fact, as the Court noted, HGS was reading from Judge Newman's concurrence-in-part and dissent-in-part. *Id.* at 12:13-14. The portions of the *dissent* relied on by HGS in the hearing were soundly rejected by the majority: "The dissent-in-part makes some points that need to be answered. First, it continually refers to an action under § 146 as being '*de novo*,' implying thereby that there are no limits on the issues that can be raised in such an action. We repeat what we noted earlier, that the statute does not contain '*de novo*' language, only stating that 'the right of the parties to take further testimony' is not prejudiced." *Conservolite*, 21 F.3d at 1103. As this Court properly noted "[d]*e novo* review can mean a whole host of things...." Transcript, Ex. F at 13:19-20. In a 146 action, the Federal Circuit has clearly stated that *de novo* review does not mean that "there are no limits on the issues that can be raised." Instead, *Conservolite* limited the right to raise new issues to "compelling circumstances" and "implicitly required the proponent of the testimony on a new issue to justify its admission in the § 146 proceeding." *Cell Genesys*, 499 F.Supp.2d at 75 (citing *Conservolite*, 21 F.3d at 1102-03). In this action, HGS has not identified a new issue that needs to be considered, let alone a compelling reason to consider a new issue.

For an issue not decided by the Board to qualify for 146 review, a party must fully present the issue through a properly filed motion during the interference. *Conservolite*, 21 F.3d at 1102 (holding that "the issue should have been raised as specified in the PTO's interference rules, for example, through preliminary motions, motions to correct inventorship, belated motions delayed for good cause, or opposition to these motions.") (citing *General Instrument*, 995 F.2d at 214. "A party may not, however, advance new legal theories at the trial court level, even if the overarching legal issue was presented below." *Boston Scientific Scimed*, 497 F.3d at 1298. "Failure to advance legal theories before the board constitutes a failure to 'make a complete presentation of the issues,' and permitting a party to raise those theories for the first time before the trial court would be both inefficient and 'wasteful of administrative and judicial resources.'" *Id.* (citation omitted).

Even for issues properly raised before the Board, the Court should exercise its discretion and not consider those issues not decided by the Board. *Brunswick Corp. v. Riegel Textile Corp.*, 627 F.Supp. 147, 153 (N.D.Ill. 1985) (holding that because the Board deemed a decision on derivation unnecessary in light of its case-dispositive holdings, derivation is not on appeal). "The desirability of the expert agency considering decisive matters relating to priority and patentability before they are raised in an action under Section 146, which is essentially an appeal subject to the right to present new evidence on issues raised, still exists." *Conservolite*, 21 F.3d at 1103. "By first allowing the Board to make factual and legal findings, the court can take advantage of the Board's specialized knowledge of the complex patent issues in dispute. Remanding to the Board any unaddressed issues in highly technical cases such as the case at bar 'would be consistent with the modern scheme of administrative law in which specialized agencies are responsible for initial decisions of complex factual and legal matters but are accountable on review to Article III judges.'" *Goliath Hundertzehnte Vermoögensverwaltungsgesellschaft mbH v. Yeda Research & Development Co.*, 2003 WL 22830014 (D.D.C. 2003) (precluding consideration of issues and evidence related to issues properly raised but not decided by the Board) (citation omitted).

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

**C. A PARTY TO A 146 ACTION CANNOT TAKE NEW DISCOVERY OR INTRODUCE NEW EVIDENCE THAT IT COULD HAVE PRESENTED TO THE BOARD**

A party is precluded from presenting evidence for the first time in a 146 action if the party did not exercise due diligence in seeking that evidence during the interference proceeding. *Cell Genesys*, 499 F.Supp.2d at 61, 73-75 (citing *Velsicol Chemical Corp. v. Monsanto Co.*, 579 F.2d 1038, 1045 (7th Cir. 1978); *Kirschke v. Lamar*, 426 F.2d 870, 874 (8th Cir. 1970); *Barrett Co. v. Koppers Co.*, 22 F.2d 395, 397 (3rd Cir. 1927)).<sup>2</sup> It is enough that a reasonably diligent preparation of a party's case below would have led to the discovery of the evidence, even evidence not in the party's exclusive possession or control. *Velsicol Chemical*, 579 F.2d at 1046 ("Velsicol failed to meet its burden with respect to the justification of its failure to present the testimony ... in the interference proceeding."). "The parties ... must make a complete presentation of the issues at the Board level so that the interference is efficient and not wasteful of administrative and judicial resources." *Conservolite*, 21 F.3d at 1102; *Velsicol Chemical Corp.*, 579 F.2d at 1045 ("The viability of the administrative process presupposes that pertinent and available testimony will be presented before the appropriate administrative body.") (citations omitted). Evidence relating to the disclosure of a patent or application should be available to a party available for presentation to the Board without the need for discovery from the opposing party. *Stamicarbon v. Chemical Construction Corp.*, 355 F.Supp. 228, 234 (D.Del. 1973) (denying motion to compel discovery related to, *inter alia*, conception, first reduction to practice, and underlying laboratory research for a patent disclosure because the "disclosure of the applications involved must speak for themselves.... [What a party] purported or intended to disclose in writings other than the application is irrelevant...."). The proponent of new evidence bears "the burden of proving that [it has] not waived the right to present this evidence." *Piher, S.A. v. CTS Corp.*, 664 F.2d 122, 125 (7th Cir. 1981) (citations omitted). *See also Cell Genesys*, 499 F.Supp.2d at 75; *Brunswick Corp.*, 627 F. Supp. at 151.

**D. THE ISSUES ON APPEAL AND THE PROPER SCOPE OF DISCOVERY IN THIS 146 ACTION**

This Court should only consider issues decided by the Board, and for those issues, preclude HGS from presenting new evidence or taking discovery.

**1. The Issue of Priority is not on Appeal**

When the Board declines to consider an issue that was not properly raised, the only issue on appeal is whether the Board abused its discretion in not considering the issue. *Credle v. Bond*, 25 F.3d 1566, 1572, n. 14 (Fed. Cir. 1994) (finding no abuse of discretion in not considering a patentability challenge that was not properly raised by preliminary motion). *See also Brunswick Corp.*, 627 F. Supp. at 151 ("the only issue relating to Riegel's alleged fraud on the Patent office that is before this court is whether the Board's conclusion precluding Brunswick from pursuing that claim is erroneous.")

<sup>2</sup> The Federal Circuit has repeatedly declined to review when a district court can properly exclude new evidence on an issue raised for consideration in a 146 action. *General Instrument*, 995 F.2d at 214 ("we again have no occasion to decide whether 'a district court may properly restrict the admission of testimony on an issue raised before the [B]oard.'") (citing *Case v. CPC Int'l, Inc.*, 730 F.2d 745, 752 (Fed. Cir. 1984)).

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

The substance of HGS and Immunex's priority cases, the second phase of a patent interference, was not presented in the interference below and was not decided by the Board. In the decision on substantive motions, the Board determined that HGS was the junior party with no patentable claims involved in the interference. D-O, Ex. D at 3:6-9. As such, HGS was put under an order to show cause why the interference should be allowed to continue and judgment should not be entered against it. *Id.* "[T]he basis for the order [to show cause] was, that the critical question of the interference has been answered and there is no longer sufficient reason to continue the interference and put the board and the parties to the expense of presenting and evaluating priority." D-O, Ex. D at 9:19-23. In response, HGS prematurely filed its priority record. O-EP, Ex. E at 3:5-9. The Board held that "HGS has failed to provide sufficient cause to continue this interference." D-O, Ex. D at 12:5. The Board noted that, contrary to HGS' request, it would not "evaluate HGS (sic) priority case to determine if [it] should consider HGS' priority case." D-O, Ex. D at 12:2-3. Because HGS prematurely filed its priority record and the interference "terminated by judgment without considering priority," the Board expunged HGS' priority record from the official PTO record. O-EP, Ex. E at 3:6-9.

While the Board's decision to not conduct the priority phase may be on appeal for abuse of discretion, priority should not be considered and no discovery related to priority should be allowed. Numerous legal issues are implicated in a priority determination including conception, diligence, and actual reduction to practice. None of these issues were fully developed, let alone decided by the Board in the interference. The priority phase is often the most fact intensive portion of an interference requiring numerous inventor depositions and consideration of not only numerous invention notebooks but also extensive expert evidence related to the meaning of this information. Consideration of priority in the first instance in the present 146 action would most likely more than double the scope of this appeal, placing a substantial burden on both parties and depriving the court of the "advantage of the Board's specialized knowledge of the complex patent issues in dispute." *Goliath*, 2003 WL 22830014.

## **2. The Board's Decision that all of HGS' Involved Claims are Unpatentable under 35 U.S.C. § 102(e) in View of Immunex's '047 Patent**

In Immunex Motion 3, Immunex requested, in part, that all of HGS' involved claims be found unpatentable under § 102(e) in view of U.S. Patent Nos. 6,072,047 ("the '047 patent"), 6,642,358 ("the '358 patent"), 6,569,642 ("the '642 patent") or International Application No. WO 98/35986 ("WO '986"). D-M, Ex. C at 29:2-10. Immunex requested judgment because Immunex's issued patents and published patent applications described the subject matter of the HGS involved claims and had an effective filing date before the HGS inventors "invented" the HGS involved claims. Because a § 102(e) motion by its nature involves the issue of when an opponent "invented" its claims, in opposition a party may (1) defer consideration of the motion to the priority phase if the party has alleged an earlier date of invention in its priority statement, or (2) oppose the motion on the merits by, for example, presenting proof of prior invention. *LeVeen v. Edwards*, 2000 WL 1862544 at \*5 (BPAI 2000) (identifying termination of the interference as a possible consequence of an unsuccessful opposition on the merits if a party is left with no patentable claims). Here, HGS made the strategic decision to oppose the motion on the merits, but did not present any evidence of prior invention or contest that "the '047 patent [or the other asserted references describe] the subject matter of its claims at issue." Decision-Rehearing, Ex. G attached hereto at 3:19-24; D-M, Ex. C at 33:4-5. Instead, the legal theory advanced by HGS was that "the '047 patent [and the other asserted references do] not qualify as

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

prior art because [HGS]' '583 application claims are said to be entitled to the benefit of the 17 March 1997 filing date of' HGS' U.S. Patent Application No. 60/040,846 ("the '846 application"). D-M, Ex. C at 33:6-9. At oral argument and following the decision on the substantive motions, HGS belatedly requested that the Board defer judgment on the motion to the priority phase. On rehearing, the Board found, *inter alia*, that HGS' request was untimely. Decision-Rehearing, Ex. G at 8:6-9:22.

Because HGS did not dispute that the disclosure of the '047 patent described all the HGS claims in the interference, the Board found that "[t]he dispositive question here is whether the [HGS] claims at issue are entitled to benefit of the 17 March 1997 filing date of [HGS]' '846 provisional application, thereby, antedating the 26 June 1997 filing date of [Immunex's] '047 patent." D-M, Ex. C at 33:23-25. The Board held that "the disclosure of the [HGS]' '846 application fails to satisfy the 'how-to-use' requirement of § 112, first paragraph, as to the subject matter of the [HGS] claims at issue. The [HGS] claims at issue are, therefore, not entitled to § 119(e) benefit of the filing date of [HGS]' '846 application." D-M, Ex. C at 37:21-38:1. The decision on appeal is the Board's ruling that HGS' involved claims are not entitled to the filing date of its '846 application. The legal theories advanced by HGS for the benefit of the filing date of the '846 application are substantially similar to the legal theories set forth in *infra* part D.3. D-M, Ex. C at 34:1-38:1.

The Board denied Immunex's motion "to the extent [the motion] seeks a judgment that any of the [involved claims] are unpatentable under § 102(a)" because none of the asserted references qualify as prior art under § 102(a). D-M, Ex. C at 31:22-32:1. The Board further denied the motion with respect to WO '986 because Immunex failed to establish that WO '986 qualifies as prior art under § 102(e). D-M, Ex. C at 32:7-11. These issues may also be on appeal.

The Board did not address Immunex's allegations of anticipation under § 102(e) in view of the '358 or '642 patents. D-M, Ex. C at 32:18-20. The Court may, but need not consider these issues.

HGS should be precluded from presenting new evidence or requesting discovery related to its allegation that the '583 application claims are entitled to the benefit of the March 17, 1997 filing date of its '846 application. HGS' allegation relates solely to the disclosure of its alleged priority application to one of ordinary skill in the art. This information is and always has been in HGS' possession and control or readily available to HGS. In opposition to Immunex Motion 3, HGS relied on 93 exhibits, presented the testimony of its expert witnesses Drs. Reed and Badley, and deposed Immunex's expert witness, Dr. Cheng. HGS requested no other discovery from Immunex to oppose the motion. No discovery by HGS was or is now necessary to resolve this issue.

### **3. The Board's Decision that HGS is not Entitled to Benefit for the Purposes of Priority of the Filing Date of the '846 Application as to Count 1**

In HGS Motion 2, HGS requested, in part, benefit for the purposes of priority of the filing date of HGS' '846 application as to Count 1. D-M, Ex. C at 7:20-23. In support, the legal theories advanced by HGS were the '846 Application describes and enables Count 1 because (1) "the similarity between the deduced amino acid sequence of DR5 and the known amino acid sequences of TNF death receptor proteins, i.e., TNFR1, Fas and DR3, as described in the '846 application is sufficient to characterize DR5 as a putative TNF death receptor protein and to

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

predict that DR5 has utilities/functions similar to those of known death receptors proteins, e.g., induction of apoptosis upon activation," D-M, Ex. C at 17:13-19; and (2) "the DR5 protein of the '846 application inherently binds TRAIL and that the '846 specification explicitly teaches that DR5 binds a TNF ligand selected from a limited list which includes TRAIL," D-M, Ex. C at 25:5-7. The Board rejected both legal theories and found the HGS '846 application does not describe and enable Count 1. D-M, Ex. C at 24:18-22, 25:5-23. The issue on appeal is the Board's decision and HGS is limited to the legal theories it advanced.

HGS should be precluded from presenting new evidence or requesting discovery related its request for benefit for the purposes of priority of the filing date of HGS' '846 application as to Count 1. HGS' request for benefit relates solely to the disclosure of its alleged priority application to one of ordinary skill in the art. This information is and always has been in HGS' possession and control or readily available to HGS. In HGS Motion 2, HGS relied on 61 exhibits, and the testimony of Dr. Reed, and deposed Immunex's expert witness, Dr. Cheng. HGS requested no other discovery from Immunex to oppose the motion. No discovery was or is now necessary to resolve this issue.

**4. The Board's Decision that Immunex is Entitled to Benefit for the Purposes of Priority of the Filing Date of the '536 and '852 Applications as to Count 1**

In Immunex Motion 1, Immunex requested, in part, benefit for the purposes of priority of the filing date of U.S. Patent Application Nos. 08/829,536 ("the '536 application") and 08/869,852 ("the '852 application") as to Count 1. D-M, Ex. C at 42:5-11. In opposition, HGS relied only on attorney argument that Immunex had not met its initial burden with respect to its motion. Specifically, HGS argued that "[n]owhere in Rauch Substantive Motion 1 does Party Rauch even imply that its earlier applications discloses [sic] a utility...." D-M, Ex. C at 46:20-22. The Board disagreed stating, *inter alia*, HGS "has not provided any basis to doubt the objective truth of the express statements in the '852 and '536 specifications...." D-M, Ex. C at 49:2-3. The issue on appeal is whether the Board correctly decided that Immunex adequately alleged a utility in motion 1 for a polypeptide within the scope of the count (TRAIL-R2).

HGS should be precluded from presenting new evidence or requesting discovery related to this issue. HGS made the strategic decision to rely solely on attorney argument that Immunex had not meet its initial burden with respect to its motion. HGS requested no discovery from Immunex to oppose the motion. No discovery by HGS was or is now necessary to resolve the issue.

**5. The Board's Decision that Immunex is not Entitled to Benefit for the Purposes of Priority of the Filing Date of the '255 and '861 Applications as to Count 1**

In Immunex Motion 1, Immunex requested, in part, benefit for the purposes of priority of the filing date of the U.S. Patent Application Nos. 08/815,255 ("the '255 application") and 08/799,861 ("the '861 application") as to Count 1. D-M, Ex. C at 42:5-11. The legal theory advanced by Immunex was that Immunex's priority applications each describe and enable Count 1, because "(a) the isolated, purified TRAIL-R protein disclosed in the '255 and '861 applications inherently has an amino acid sequence at least 90% identical to that set forth in SEQ ID NO:2 of the '358 patent and (b) the '255 and '861 applications disclose that TRAIL-R binds TRAIL." D-M, Ex. C at 51:13-17. The Board found that "[Immunex] has failed to establish that the isolated, purified TRAIL-R protein disclosed in the '255 and '861 applications inherently has an amino

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

acid sequence at least 90% identical to that set forth in SEQ ID NO:2 of the '358 patent." D-M, Ex. C at 56:17-19. The Board also found that the '255 and '861 applications disclose a utility for TRAIL-R. D-M, Ex. C at 56:21-57:3.<sup>3</sup> The issue on appeal is whether the Board correctly decided that the isolated, purified TRAIL-R protein disclosed in Immunex's '255 and '861 applications does not inherently have an amino acid sequence at least 90% identical to that set forth in SEQ ID NO:2 of the '358 patent.

HGS should be precluded from presenting new evidence or requesting discovery related to Immunex's request for benefit for the purposes of priority of the filing date of the '255 application and the '861 application. The legal theories advanced by HGS in opposition relate solely to the disclosure of Immunex's priority applications to one of ordinary skill in the art. This information is and always has been in HGS' possession and control or readily available to HGS. In opposition to Immunex Motion 1, HGS relied on 44 exhibits, and the testimony of Dr. Badley, and deposed Immunex's expert witness, Dr. Cheng. HGS requested no other discovery from Immunex to oppose the motion. No discovery was or is now necessary to resolve this issue.

#### **6. The Board's Decision That HGS Failed to Show its Best Proofs are Outside the Scope of the Count**

In HGS Motion 1, HGS requested to substitute Count 1 with its proposed Count 2. D-M, Ex. C at 4:22-24. HGS argued in support of the motion that its best proofs did not expressly recite the "binding TRAIL" limitation of Count 1 and proposed changing the count to include the property of "inducing apoptosis." D-M, Ex. C at 5:23-26. HGS asserted that "the abilities to bind TRAIL and to induce apoptosis are inherent properties of the polypeptide of Count 1." D-M, Ex. C at 5:9-10. The Board determined that HGS "has failed to demonstrate that its best proofs are outside the scope of the current count and, therefore, that there is a genuine need to change the count." D-M, Ex. C at 7:6-8. The issue on appeal is whether the Board correctly decided that HGS failed to demonstrate that there is a genuine need to change the count.<sup>4</sup>

HGS should be precluded from presenting new evidence or requesting discovery related to its request to substitute the Count. HGS' allegation relates solely to its own best proofs of priority and whether those best proofs are outside the scope of the Count. This information is and always has been in HGS' possession and control or readily available to HGS. HGS submitted no documents or testimony to support the contention that its best proofs did not expressly recite the express property of the count of "binding TRAIL." No discovery was or is necessary to resolve this issue.

#### **7. The Board's Decision that Immunex's Involved Claims are Patentable over HGS' '568 Patent**

In HGS Motion 3, HGS alleged that Immunex's involved claims are unpatentable under § 102(e) as anticipated by U.S. Patent No. 6,872,568 ("the '568 patent"). D-M, Ex. C at 57:14-

<sup>3</sup> HGS advanced the same attorney argument for utility set forth in *supra* part D.4.

<sup>4</sup> Both Immunex and HGS contingently moved for benefit for the purposes of priority of several previously filed applications in the event the Board granted HGS' motion to modify the count. The Board dismissed both motions as moot because the Board denied HGS' motion to substitute the Count. Both contingent motions should be remanded to the Board in the event the Court reverses the Board's decision to substitute the count.

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
 United States District Court of Delaware  
 December 5, 2007

18. Though the HGS '568 Patent was filed after the uncontested effective filing date of Immunex's involved claims, D-M, Ex. C at 64:1-9, HGS alleged that the '568 patent was entitled, for prior art purposes, to the filing date of several earlier filed applications. Because HGS "neither argued nor pointed out where the antibody-based subject matter claimed in the '568 patent is disclosed in" any of the several earlier filed applications as required, D-M, Ex. C at 61:3-5, the Board found that the HGS '568 patent did not qualify as prior art under § 102(e). D-M, Ex. C at 64:10-13. The Board's decision was based on HGS' complete failure to present any evidence or argument for a key element required by its motion. The issue on appeal is whether the Board correctly denied the motion because HGS failed to present any evidence or argument why the '568 patent should be entitled to an earlier effective date.

Because the Board found that the HGS '568 patent did not qualify as prior art under § 102(e), the Board did not consider the content of the HGS '568 patent or Immunex's assertion of an earlier filing date for its involved claims. D-M, Ex. C at 64:10-18. The Court may, but need not, consider these issues.

HGS should be precluded from presenting new evidence or requesting discovery related to its allegation for benefit for prior art purposes. HGS' allegation relates solely to the objective teaching of its alleged priority application to one of ordinary skill in the art. This information is and always has been in HGS' possession and control or readily available to HGS. In HGS Motion 3, HGS relied on 74 exhibits, and the testimony of Drs. Reed and Badley, and deposed Immunex's expert witness, Dr. Cheng. HGS requested no other discovery from Immunex related to the motion. No discovery was or is necessary to resolve the issue on appeal. HGS should not now be allowed to present evidence or make arguments that it should have and could have presented to the Board.

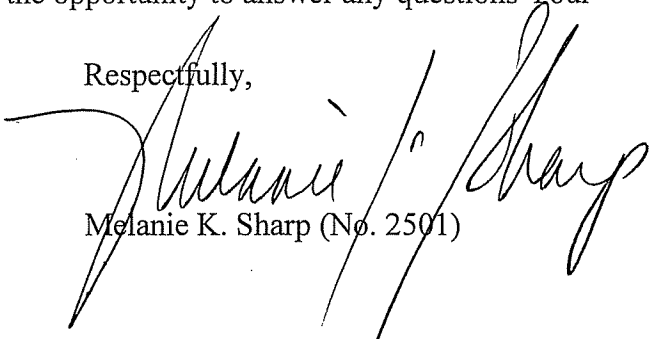
#### **8. Immunex and HGS' Motions to Suppress Evidence**

Both HGS and Immunex filed evidentiary motions to exclude evidence submitted to the Board. D-M, Ex. C at 2:11; 2:22. The Board denied HGS' motion because, *inter alia*, the "motion has serious procedural defects." D-M, Ex. C at 68:38. The Board's denial of HGS' evidentiary motion is on appeal for abuse of discretion. The Board also dismissed Immunex's motion as moot. D-M, Ex. C at 101:3-5. The Court may, but need not, consider Immunex's evidentiary motion. No new evidence or discovery is appropriate regarding the Court's review of the Board's evidentiary rulings.

### **III. CONCLUSION**

Immunex requests this Court to rule that the issue of priority, *i.e.*, the acts of invention such as conception, actual reduction to practice, and diligence, is not on appeal. Immunex requests that the Court limit the present action to issues decided by the Board and the legal theories presented supporting those issues. Immunex further requests that discovery be limited as set forth herein. Immunex would welcome the opportunity to answer any questions Your Honor might have regarding these issues.

Respectfully,

  
 Melanie K. Sharp (No. 2501)

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
United States District Court of Delaware  
December 5, 2007

MKS

cc: Clerk of the Court (Hand Delivery)  
John G. Day, Esquire (via e-mail)  
Steven J. Balick, Esquire (via e-mail)  
Lauren E. Maguire, Esquire (via e-mail)

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL

**EXHIBIT A**

Paper 4

Filed by: Richard E. Schafer  
Administrative Patent Judge  
Mail Stop Interference  
P.O. Box 1450  
Alexandria Va 22313-1450  
Tel: 571-272-9797  
Fax: 571-273-0042

Filed: October 5, 2005

UNITED STATES PATENT AND TRADEMARK OFFICE

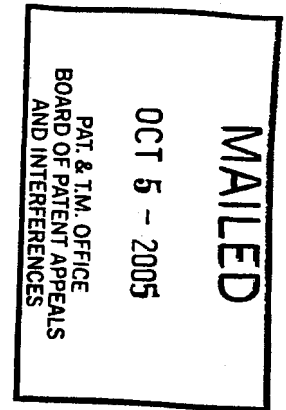
BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES  
(Administrative Patent Judge Richard E. Schafer)

**Human Genome Sciences, Inc.,**  
Junior Party  
(Application 10/005,842-IFW  
Inventors: Jian Ni, Reiner L. Gentz,  
Guo-Liang Yu and Craig A. Rosen),

v.

**Immunex Corp.,**  
Senior Party  
(Patent 6,642,358  
Inventors: Charles Rauch and Henning Walczak).

Patent Interference No. 105,381 (RES)



**Order - Preliminary Motion Times - Bd. R. 104(c)**  
(Setting preliminary motion times)

This order applies to motions, if any, authorized as the result of the conference call scheduled for **November 21, 2005** (Paper 1). 37 CFR § 41.121(a)(1) and (2).

**A. Time periods associated with motions**

The TIME PERIODS described below are set out in an Appendix to this ORDER. Action specified for each TIME PERIOD must be completed by the date specified for the TIME PERIOD.

The parties are authorized to stipulate different times (earlier or later, but not later than TIME PERIOD 7) for TIME PERIODS 1 through 6.<sup>1</sup> A notice of the stipulation must be promptly filed. The notice must be in the form of a photocopy of the Appendix attached to this ORDER with old

<sup>1</sup> In stipulating different times, the parties should consider the effect of the stipulation on times (1) to object to evidence (5 business days, Bd. R. 155(b)(1)), (2) to supplement evidence (10 business days, Bd. R. 155(b)(2)), (3) to begin cross examination (no earlier than 21 days after service, SO ¶ 22.1.1) and (4) to conclude cross examination (at least 10 days before opposition or reply is due, SO ¶ 22.1.2).

Letter Brief  
Ex. A  
Order-Motion Times

dates crossed out and new dates inserted by hand. The parties may not stipulate an extension of TIME PERIODS 7-8.

**1. TIME PERIOD 1**

- a. File and serve all authorized motions and
- b. Serve but do not file evidence in support of these motions.

If no party files a motion, the SENIOR PARTY must arrange a conference call with the parties and the Board so that appropriate adjustments to the schedule may be made.

**2. TIME PERIOD 2**

- a. File and serve responsive motions (Bd. R. 121(a)(2)) in response to an opponent's motion filed during TIME PERIOD 1 and
- b. Serve but do not file evidence in support of these responsive motions.

**3. TIME PERIOD 3**

- a. File and serve oppositions to all motions, including responsive motions and
- b. Serve but do not file evidence in support of these oppositions.

**4. TIME PERIOD 4**

- a. File and serve replies to all oppositions and
- b. Serve but do not file evidence in support of these replies.

**5. TIME PERIOD 5**

- a. File and serve any request for oral argument on motions,
- b. File and serve motions to exclude objected to evidence (Bd. R. 155(c); SO ¶ 21.3), and
- c. File and serve observations on cross examination (SO ¶ 22.7) of reply testimony.

**6. TIME PERIOD 6**

- a. File and serve oppositions to an opponent's motion to exclude evidence and
- b. File and serve any response to observations.

**7. TIME PERIOD 7**

File and serve replies to oppositions to motions to exclude evidence.

**B. Deposition transcripts**

Transcripts of cross examinations and depositions taken under 35 U.S.C. § 24 must be served, but not filed until the exhibits are filed.

**C. Serving exhibits relied upon in motions**

An exhibit, including an affidavit, cited in connection with a motion, opposition, reply, or affidavit, must be served, but not filed,<sup>2</sup> with the motion, opposition, reply or affidavit in which the exhibit is first mentioned.

**D. TIME PERIOD 8: Filing the record for decision on motions**

1. File an original set of your exhibits and one working copy (or three copies if an oral argument is set) of your exhibits;
2. For each of your motions, file one folder (or three folders if an oral argument is set each) containing:
  - a. The motion,
  - b. Any corresponding opposition,
  - c. Any corresponding reply,
  - d. Any corresponding observations, and
  - e. Any corresponding response to the observations.
3. File any ZIP® 100 Mb disk or CD-ROM a party elects to file.

**E. Priority statements**

1. At TIME PERIOD 1:
  - a. File but do not serve a priority statement (Bd. R. 120; Bd. R. 204(a)).
  - b. File and serve a notice advising each opponent of the filing of the priority statement.
2. A junior party who does not file a priority statement shall not have access to the priority statement of any other party.
3. **Within one (1) week** after TIME PERIOD 1, serve a copy of the priority statement upon each opponent (except for a junior party barred under ¶ H.2 above).

---

/Richard E. Schafer/  
Administrative Patent Judge

---

<sup>2</sup> Except when the Board sets an expedited schedule for a particular motion, in which case, all exhibits mentioned in that motion or the corresponding opposition or reply must be filed with the motion, opposition, reply, or affidavit in which the exhibit is first mentioned.

cc (via overnight delivery):

Attorney for Human Genome Sciences:

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
1100 New York Avenue, N.W.  
Washington, DC 20005  
(202)371-2600

Attorney for Immunex:

IMMUNEX CORPORATION  
Law Department  
1201 Amgen Court West  
Seattle, WA 98119  
(206)265-7000

**Appendix--ORDER - RULE 123(a)**  
**(Times for substantive motions; priority deferred)**

Interference 105,381(RES)

TIME PERIOD 1 .....	<b>January 9, 2006</b>
File motions	
File (but serve one week later) priority statements	
TIME PERIOD 2 .....	<b>January 30, 2006</b>
File responsive motions to motions	
filed in TIME PERIOD 1	
TIME PERIOD 3 .....	<b>March 13, 2006</b>
File oppositions to all motions	
TIME PERIOD 4 .....	<b>April 24, 2006</b>
File all replies	
TIME PERIOD 5 .....	<b>June 5, 2006</b>
File request for oral argument	
File motions to exclude	
File observations	
TIME PERIOD 6 .....	<b>June 26, 2006</b>
File oppositions to motions to exclude	
File response to observations	
TIME PERIOD 7 .....	<b>July 10, 2006</b>
File replies to oppositions to motions to exclude	
TIME PERIOD 8 .....	<b>July 17, 2006</b>
File exhibits	
File sets of motions	
File any ZIP® disks or CD-ROMs	

**Appendix II--ORDER - RULE 123(a)**

**(Times for substantive motions)**

Interference 105,381 (RES)

**I. Required Appendices**

**1. List of exhibits**

The list of exhibits cited in support of a motion, opposition, or reply, SO ¶¶ 13.3(b) & 14.3(a), must be set forth as an appendix to the motion, opposition, or reply, respectively. The appendix will not count against the page limit for the motion, SO ¶ 13.2, or opposition or reply, SO ¶ 14.2.

**2. Statement of Material Facts**

The statement of proposed material facts for each motion, opposition, or reply must be set forth as an appendix to the motion, opposition, or reply, respectively. Bd.R. 121(d)(2). The appendix will not count against the page limit for the motion, SO ¶ 13.2, or opposition or reply, SO ¶ 14.2.

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL

**EXHIBIT B**

Paper 103

Filed: 9 April 2007

Mail Stop Interference  
P.O. Box 1450  
Alexandria Va 22313-1450  
Tel: 571-272-4683  
Fax: 571-273-0042

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES  
(Administrative Patent Judge Richard E. Schafer)

**Human Genome Sciences, Inc.,**  
Junior Party  
(Application 10/005,842-IFW  
Inventors: Jian Ni, Reiner L. Gentz,  
Guo-Liang Yu and Craig A. Rosen),

v.

**Immunex Corp.,**  
Senior Party  
(Patent 6,642,358  
Inventors: Charles Rauch and Henning Walczak).

Patent Interference No. 105,381 (RES)

**Order - Miscellaneous - Bd.R. 104(a)**

A telephone conference call was held on April 3, 2007 at approximately 10:30  
a.m., involving:

Letter Brief  
Ex. B  
Order-Miscellaneous

- 1
- 2 1. Jorge A. Goldstein, Esq. and Eldora Ellison, Esq., counsel for Human
- 3 Genome Sciences (HGS),
- 4 2. Michael J. Wise, Esq., counsel for Immunex, and
- 5 3. Richard E. Schafer, Administrative Patent Judge.

6 The conference call was requested by HGS.

7 HGS requested permission to file a miscellaneous motion seeking additional  
8 discovery on the inventorship of its involved applications, permission to file a modified  
9 priority statement, to modify the priority schedule and/or to synchronize the times in this  
10 interference and Interference 105,380 with the times in Interference 105,361.

11 The request to file a motion for additional discovery on HGS' inventorship was  
12 denied. The inventorship of HGS' involved applications is not at issue in these  
13 interferences. If HGS finds that it needs to change the inventorship of its applications, it  
14 may attempt to do so when its application returns to the jurisdiction of the Commissioner  
15 of Patents. For the purposes of these interferences, the inventor ship is as stated in HGS  
16 involved application. However, in order to provide HGS with an opportunity to further  
17 investigate the inventorship question, the schedule will be adjusted an additional month  
18 and is reset in the appendix to this order. The conference call to discuss the priority  
19 schedule set for April 26, 2007 at 4:00 p.m. is cancelled.

20 The request to synchronize the times in this interference with the times in  
21 Interference 105,361 was also denied. HGS sought synchronization because of a  
22 concern that the opposing party in Interference 105,361 (Genentech) would be given an  
23 unfair advantage by having access to HGS' priority proofs. Interference 105,361 is  
24 currently awaiting a decision on substantive motions and has not entered the priority  
25 phase. Synchronizing the files would require suspending the priority schedule in these  
26 interferences. It was also suggested that Genentech be precluded from having access to  
27 HGS priority case. However, these interferences are open to the public and to preclude

1 access by Genentech would require precluding public access to this interference.

2 HGS also requests submitted an amended priority statement. This was also  
3 denied. However, HGS was authorized, as part of its priority case to submit proofs of an  
4 actual reduction to practice by March 25, 1997.

5 Immunex raised a question relating the continuance of this interference into the  
6 priority phase in light of the fact that all of HGS' claims corresponding to the count in  
7 were held to be unpatentable. This matter is currently under consideration.

8  
9 /Richard E. Schafer/  
10 Administrative Patent Judge  
11  
12  
13

14 cc (electronic filing):

15 Counsel for HUMAN GENOME SCIENCES, INC.

16  
17 Jorge Goldstein, Esq.  
18 STERNE, KESSLER, GOLDSTEIN & FOX PLLC  
19 1100 New York Avenue, N.W.  
20 Washington, D.C. 20005-3934  
21 Tel: 202-371-2600  
22 Email: [jgold@skgf.com](mailto:jgold@skgf.com)  
23  
24

25 Counsel for IMMUNEX CORP.

26  
27 Michael J. Wise, Esq.  
28 PERKINS COIE LLP  
29 1620 26<sup>th</sup> Street  
30 6<sup>th</sup> Floor, South Tower  
31 Santa Monica, CA 90404-4013  
32 Tel: 310-788-3210  
33 Email: [mwise@perkinscoie.com](mailto:mwise@perkinscoie.com)

Letter Brief  
Ex. B  
Order-Miscellaneous

**Appendix--ORDER - RULE 123(a)**  
**(Times for priority motions)**  
Interference 105,381 (RES)

TIME PERIOD 11.....**July 6, 2007**

Junior party only file priority motion and serve  
(but do not file) priority evidence

TIME PERIOD 12.....**August 17, 2007**

Senior party only file priority motion and serve  
(but do not file) priority evidence

TIME PERIOD 13.....**September 28, 2007**

File opposition to priority motions  
Serve (but do not file) opposition evidence

TIME PERIOD 14.....**November 9, 2007**

File reply  
Serve (but do not file) reply evidence

TIME PERIOD 15.....**December 21, 2007**

Request oral argument  
File list of issues to be considered  
File observations  
File motion to exclude

TIME PERIOD 16.....**January 11, 2008**

File response to observations  
File opposition to motion to exclude

TIME PERIOD 17.....**January 25, 2008**

File reply to opposition to motion to exclude

TIME PERIOD 18.....**February 01, 2008**

File and serve exhibits  
File sets of priority motions  
File CD-ROMs

TIME PERIOD 19.....**Ferburary 29, 2008**

Default oral argument date (if ordered)

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL  
**EXHIBIT C**

The opinion in support of the decision being  
entered today is not binding precedent of the Board.

Paper 101

By: Trial Section Merits Panel  
Board of Patent Appeals and Interferences  
Mail Stop Interference  
P.O. Box 1450  
Alexandria, VA 22313-1450  
Tel: 571-272-9797  
Fax: 571-273-0042

Filed: March 26, 2007

UNITED STATES PATENT AND TRADEMARK OFFICE

---

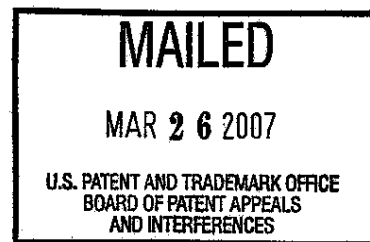
BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES  
(Administrative Patent Judge Richard E. Schafer)

---

**Human Genome Sciences, Inc.**  
Junior Party  
(Application 10/005,842-IFW  
Inventors: Jian Ni, Reiner L. Gentz,  
Guo-Liang Yu and Craig A. Rosen),

v.

**Immunex Corp.,**  
Senior Party  
(Patent 6,642,358  
Inventors: Charles Rauch and Henning Walczak)



---

Patent Interference No. 105,381 (RES)

---

Before: SCHAFFER, HANLON and SPIEGEL, Administrative Patent Judges.

SPIEGEL, Administrative Patent Judge.

**DECISION - MOTIONS - Bd.R. 125(a)**

Letter Brief  
Ex. C  
D-M

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 2  
Paper 101

1     **I.     Introduction**

2             This is a decision on the motions remaining in interference no. 105,381.

3             Junior party Ni has filed four motions. Senior party Rauch has filed five  
4     motions.

5             Ni substantive motion 1 to substitute Ni proposed count 2 for current  
6     Count 1 is **denied**. Ni substantive motion 2 for benefit for the purpose of priority  
7     is **dismissed** as moot as to Ni proposed count 2, **granted** as to the 29 July 1997  
8     filing date of the 60/054,021 application for Count 1 and otherwise **denied**. Ni  
9     substantive motion 3 seeking judgment that all Rauch's involved claims are  
10    unpatentable under 35 U.S.C. § 102(e) as anticipated by U.S. Patent 6,872,568  
11    is **denied**. Ni miscellaneous motion 4 to exclude certain evidence is **denied**.

12            Rauch substantive motion 1 for benefit for the purpose of priority as to  
13    Count 1 is **granted** as to the 28 March 1997 and 4 June 1997 filing dates of  
14    applications 08/829,536 and 08/869,852, respectively, and otherwise **denied**.  
15    Rauch substantive motion 2 to designate Ni claims 46, 55, 63, 64, 110 and 118  
16    as corresponding to Count 1 is **denied**. Rauch substantive motion 3 is **granted**  
17    to the extent that Ni claims 35, 36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-  
18    109, 111-116, 127-133, 168-178 and 180-203 are unpatentable under 35 U.S.C.  
19    § 102(e) as anticipated by U.S. Patent 6,072,047, **moot** as to anticipation under  
20    § 102(e) by U.S. Patents 6,642,358 and 6,569,642, and otherwise **denied**.  
21    Rauch responsive motion 4 is **dismissed** as moot in view of the denial of Ni  
22    substantive motion 1. Rauch miscellaneous motion 5 to exclude certain  
23    evidence is **dismissed** as moot.

**II. Findings of Fact (FF)**

The following findings of fact are supported by a preponderance of the evidence.

1. The junior party is Jian NI, Reiner L. GENTZ, Guo-Liang YU and Craig A. Rosen ("Ni").
2. Ni is involved in the interference on the basis of application 10/005,842 ("the '842 application," NX 2025), filed 7 December 2001.
3. The '842 application has been accorded benefit for the purpose of priority of the 17 March 1998 filing date of application 09/042,583 ("the '583 application," NX 2024).
4. Ni's real party-in-interest is Human Genome Sciences, Inc. ("HGS").
5. The senior party is Charles RAUCH and Henning WALCZAK ("Rauch").
6. Rauch is involved in the interference on the basis of U.S. Patent 6,642,358 ("the '358 patent," RX 1012), issued 4 November 2005, based on application 09/578,392 ("the '392 application"), filed 25 May 2000.
7. The '392 application has been accorded benefit for the purpose of priority of the 26 June 1997 filing date of application 08/883,036 ("the '036 application," RX 1018), which issued 6 June 2000 as U.S. Patent 6,072,047 ("the '047 patent," RX 1048)
8. Rauch's real party-in-interest is Immunex Corp. ("Immunex").
9. The subject matter of the interference is defined by one count.
10. Count 1 is "Claim 6 of U.S. Patent 6,642,358" (Paper 1, p. 3).
11. Claim 6 of the '358 patent, written in independent form, reads:

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 4  
Paper 101

1 A purified TRAIL-R polypeptide comprising an amino  
2 acid sequence that is at least 90% identical to the  
3 amino acid sequence presented in SEQ ID NO:2  
4 wherein said polypeptide binds TRAIL.

5 12. According to the '358 patent, SEQ ID NO:2 is the 440 amino acid  
6 sequence of a full length human receptor protein (including the N-  
7 terminal signal peptide), "TRAIL-R," encoded by the DNA of SEQ ID  
8 NO:1 (RX 1012, c. 1, I. 66 - c. 2, I. 2 and c. 22, II. 7-11).

9 13. The claims of the parties are:

10	Ni	35-72, 75, 83, 92, 99-133, 152-178 and 180-203
11	Rauch	1-41

12 14. The claims of the parties which correspond to Count 1 are:

13	Ni	35, 36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-
14		109, 111-116, 127-133, 168-178 and 180-203
15	Rauch	1, 4-6, 8-11, 17-19, 26-28, 34, 37, 38 and 40

16 15. The claims of the parties which do not correspond to Count 1, and  
17 therefore are not part of this interference, are:

18	Ni	37, 46, 55, 62-72, 101, 110, 117-126 and 152-167
19	Rauch	2, 3, 7, 12-16, 20-25, 29-33, 35, 36, 39 and 41

20 Other findings of fact follow below.

### 21 **III. Ni Substantive Motion 1**

22 Pursuant to 37 CFR § 41.121(a)(1)(i), Ni moves to redefine the scope of  
23 the interference by substituting proposed count 2 for current Count 1 (Paper 29).  
24 Rauch opposes (Paper 52); Ni replies (Paper 60).

25 16. Ni's proposed count 2 reads (Paper 29, p. 1, ¶ 1):

26 A purified TRAIL-R polypeptide comprising an amino  
27 acid sequence that is at least 90% identical to the  
28 amino acid sequence presented in SEQ ID NO:2

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 5  
Paper 101

1                    wherein said polypeptide binds TRAIL or induces  
2                    apoptosis.

3            17. According to Ni, its proposed count 2 simply incorporates Rauch claims 5  
4            and 6, as does the current count, and adds the language "or induces  
5            apoptosis" (id.).

6            It is our understanding that the source of SEQ ID NO:2 in Ni's proposed  
7            count 2 is the involved '358 patent of Rauch. With this understanding, we now  
8            address Ni motion 1.

9            Ni argues that the abilities to bind TRAIL and to induce apoptosis are  
10           inherent properties of the polypeptide of Count 1, although only the former is  
11           expressly recited in the count (Paper 29, p. 7, ¶ 3). A party seeking to change  
12           the count in an interference must demonstrate a genuine need to change the  
13           count. As stated in Louis v. Okada, 59 USPQ2d 1073, 1076 (Bd. Pat. App. & Int.  
14           2001),

15                                [a]t a minimum, ... a preliminary motion to  
16                                broaden out the count on the basis that a party's best  
17                                or earliest proofs are outside the current count (1)  
18                                should make a proffer of the party's best proofs, (2)  
19                                show that such best proofs indeed lie outside of the  
20                                scope of the current count, and (3) further show that  
21                                the proposed new count is not excessively broad with  
22                                respect to what a party needs for its best proofs.

23            Ni seeks to change the count by adding the limitation "or induces  
24            apoptosis" as an alternative to the limitation "binds TRAIL" (FF 16). Ni seeks to  
25            change the current count because its best proofs do not explicitly recite that the  
26            TRAIL-R polypeptide of the count binds TRAIL (FF 18). However, the fact that  
27            Ni's "best proofs" do not explicitly recite the language of the count does not alone

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 6  
Paper 101

1 establish that those proofs are not directed to "subject matter" defined by the  
2 count. "The invention is not the language of the count but the subject matter  
3 thereby defined." Silvestri v. Grant, 496 F.2d 593, 598, 181 USPQ 706, 709  
4 (CCPA 1974). In appropriate circumstances, express limitations of the count  
5 may be shown to be inherent in the proofs, id. ("In reaching this conclusion, we  
6 do not disregard the fact that the count also requires that the ampicillin  
7 possesses greater storage-stability than hydrated ampicillin and have a  
8 molecular weight of about 349. However, we regard these as inherent properties  
9 of Form II ampicillin which add nothing to the count definition beyond that  
10 determined by the [other limitations].").<sup>1</sup> The limitation said not to be disclosed  
11 by Ni's best proofs, i.e., the ability to bind TRAIL, may be shown to be an  
12 inherent property of the TRAIL-R polypeptide of the count. In fact, Ni argues that  
13 the ability to bind TRAIL and the ability to induce apoptosis are both inherent  
14 properties of the TRAIL-R polypeptide of the count:

15           The ability to bind TRAIL is an expressly recited  
16           property of the polypeptide and it is an inherent  
17           property of the polypeptide of SEQ ID NO:2.  
18           Similarly, the ability of the polypeptide of SEQ ID  
19           NO:2 to induce apoptosis is also an inherent property  
20           of the polypeptide of SEQ ID NO:2.

21 [Paper 29, p. 7, ¶ 3 (citation to material facts omitted).] Additionally, Ni has not  
22 asserted that there are polypeptides meeting the amino acid sequence

---

<sup>1</sup> In Silvestri, the count was directed to a new crystalline form of ampicillin which was "substantially free of water in the chemically bound state" and had a molecular weight of about 349, a particular infrared ("IR") spectrograph and improved storage stability vis-à-vis the previously known form of ampicillin. Id., 496 F.2d at 595-96, 181 USPQ at 709-710. The court held that it was sufficient to possess the claimed compound and to characterize it by its water content and IR spectrograph, without demonstrating the knowledge of the ampicillin's molecular weight because the molecular weight "add[s] nothing to the count beyond that determined by the water content and infrared spectrograph." Id., 496 F.2d at 599, 181 USPQ at 709.

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 7  
Paper 101

1 requirements of the count which would induce apoptosis, but not bind TRAIL.  
2 Consequently, adding the phrase "or induces apoptosis" to Count 1 has not been  
3 shown to be necessary to encompass Ni's best proofs. Furthermore, changing  
4 the scope of the count would leave Ni in essentially the same position it is in now  
5 of having to prove an inherent property of the TRAIL-R polypeptide of the count  
6 (FF 18). Hence, Ni has failed to demonstrate that its best proofs are outside the  
7 scope of the current count and, therefore, that there is a genuine need to change  
8 the count.

9 Based on the foregoing, Ni substantive motion 1 is **denied**.

#### 10 **IV. Rauch Responsive Motion 4**

11 Pursuant to 37 CFR § 41.121(a)(2), Rauch moves to be accorded benefit  
12 for the purpose of priority of the (i) 26 June 1997, (ii) 4 June 1997, (iii) 28 March  
13 1997, (iv) 12 March 1997 and (v) 13 February 1997 filing dates of U.S.  
14 applications (i) 08/883,036, (ii) 08/869,852, (iii) 08/829,536, (iv) 08/815,255 and  
15 (v) 08/799,861, respectively, as to Ni's proposed count 2 (Paper 45). Rauch  
16 responsive motion 4 is contingent upon the grant of Ni substantive motion 1 to  
17 substitute Ni's proposed count 2 for current Count 1. Since the contingency has  
18 not occurred, Rauch responsive motion 4 is **dismissed** as moot.

#### 19 **V. Ni Substantive Motion 2**

20 Pursuant to 37 CFR §41.121(a)(1)(ii), Ni moves to be accorded benefit for  
21 the purpose of priority of the 17 March 1997 and 29 July 1997 filing dates of its  
22 earlier filed provisional applications 60/040,846 ("the '846 application," NX 2042)  
23 and 60/054,021 ("the '021 application," NX 2056), respectively, as to Count 1

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 8  
Paper 101

1 and, contingent on the grant of Ni substantive motion 1, as to Ni's proposed  
2 count 2 (Paper 30). Rauch opposes (Paper 53); Ni replies (Paper 61).

3 To the extent Ni substantive motion 2 is contingent upon the grant of Ni  
4 substantive motion 1, it is **dismissed** as moot because the contingency has not  
5 occurred.

6 As discussed above, the subject matter of Count 1 is directed to a purified  
7 TRAIL-R polypeptide having an amino acid sequence that is at least 90%  
8 identical to SEQ ID NO:2 of Rauch's involved '358 patent, wherein the  
9 polypeptide binds TRAIL (FF 11).

10 18. TRAIL (TNF-Related Apoptosis-Inducing Ligand) is a member of the TNF  
11 ligand family known to be capable of inducing apoptosis when added to  
12 certain cells, e.g., Jurkat cells (NX 2096<sup>2</sup>).

13 19. The '021 and '846 application are both provisional applications.

14 20. The '021 application was filed 29 July 1997 (NX 2056, cover sheet).

15 21. The '846 application was filed 17 March 1997 (NX 2042, cover sheet).

16 22. Figure 1 of the '021 application is said to show the nucleotide and  
17 deduced amino acid sequences of "human Death Domain Containing  
18 Receptor 5" (DR5) obtained from the cDNA clone deposited as ATCC  
19 Deposit No. 97920 on 7 March 1997 (NX 2056, p. 1, ll. 7-9; p. 6, ll. 5-6; p.  
20 7, ll. 29-33; p. 9, ll. 9-12; p. 10, ll. 34-35).

21 23. According to the '021 specification, DR5 is a 411 amino acid protein (id.,  
22 p. 26, ll. 9-10).

---

<sup>2</sup> Wiley et al., "Identification and Characterization of a New Member of the TNF Family that Induces Apoptosis," Immunity, Vol. 3, pp. 673-682 (December 1995) (NX 2096).

- 1        24. Example 6 of the '021 specification is said to show that a DR5  
2        extracellular domain-Fc fusion construct (DR5-Fc) binds TRAIL (id., p.  
3        50, l. 6 - p. 51, l. 2; Figures 6A-6C).
- 4        25. Figure 1 of the '846 application is said to show the nucleotide and  
5        deduced amino acid sequences of DR5 obtained from the cDNA clone  
6        deposited as ATCC Deposit No. 97920 on 7 March 1997 (NX 2042, p. 1,  
7        ll. 5-6; p. 3, ll. 22-25; p. 5, ll. 24-27).
- 8        26. According to the '846 specification, DR5 is a 411 amino acid protein (id.,  
9        p. 6, ll. 25-27).
- 10       27. Figure 2 of the '846 application is said to compare the deduced amino  
11       acid sequence of DR5 to the amino acid sequences of three known TNF  
12       family death receptor proteins -- human tumor necrosis factor receptor 1  
13       (human TNFR1), human Fas protein and DR3 protein (id., p. 5, ll. 8-13).
- 14       28. According to the '846 specification, similarities between the amino acid  
15       sequences shown in Figure 2 "**strongly suggest** that DR5 is also a  
16       death domain containing receptor with the ability to induce apoptosis,"  
17       i.e., that DR5 is a putative death receptor protein of the TNF receptor  
18       family (id., p. 6, ll. 31-33, emphasis added).
- 19       29. Further according to the '846 specification, "TNF-family ligands induce  
20       various cellular responses by binding to TNF-family receptors, including  
21       the DR5 of the present invention. Cell which express the DR5  
22       polypeptide **are believed to have** a potent cellular response to DR5  
23       ligands ... " (id., p. 26, ll. 12-15, emphasis added).

- 1           30. The '846 specification defines "TNF-family ligand" as  
2           naturally occurring, recombinant, and synthetic  
3           ligands that are capable of binding to a member of the  
4           TNF-receptor family and inducing the ligand/receptor  
5           signaling pathway. Members of the TNF ligand family  
6           include, but are not limited to, **DR5 ligands**, TRAIL,  
7           TNF- $\alpha$ , lymphotoxin- $\alpha$  (LT- $\alpha$ , also known as TNF- $\beta$ ),  
8           LT- $\beta$  (found in complex heterotrimer LT- $\alpha$ 2- $\beta$ ), FasL,  
9           CD40, CD27, CD30, 4-1BB, OX40 and nerve growth  
10          factor (NGF). [*Id.*, p. 31, ll. 4-9, emphasis added.]
- 11          31. The amino acid sequence of the DR5 protein shown in the respective  
12          Figures 1 of the '021 and '846 applications are identical.
- 13          32. It is undisputed that the amino acid sequences shown in Figures 1 of the  
14          '021 and '846 applications are at least about 93% identical to the amino  
15          acid sequence of SEQ ID NO:2 as recited in Count 1, with 411 of 440  
16          total amino acids being identical (see Paper 53, p. 22 where Rauch  
17          admits Ni's Statement of Material Facts (SMFs) 7 and 8 as set forth in  
18          Paper 30, p. 26).
- 19          33. Thus, the '021 application describes an enabled embodiment within the  
20          scope of Count 1, i.e., a DR5 polypeptide having an amino acid  
21          sequence that is at least 90% identical to the amino acid sequence of  
22          SEQ ID NO:2 of the '358 patent (FFs 22, 31 and 32) and which binds  
23          TRAIL (FF 24).
- 24          34. Rauch does not dispute Ni's claim to benefit for the purpose of priority of  
25          the filing date of the '021 application (Paper 53).
- 26          Based on the foregoing, we accord Ni benefit for the purpose of priority of  
27          the filing date of the '021 application as to Count 1.

1 While the '846 application describes (Figure 1) a DR5 polypeptide having a  
2 deduced amino acid sequence which is at least 90% identical to the amino acid  
3 sequence set forth in SEQ ID NO:2 of the '358 patent (FF 32), the disclosure of  
4 the '846 application suggests that the DR5 polypeptide is a death domain  
5 containing receptor with the ability to induce apoptosis (FF 28). However, the  
6 disclosure of the '846 application does not describe preparing a DR5 polypeptide  
7 (or ligand binding portion thereof) or binding the ligand TRAIL to the DR5  
8 polypeptide (or ligand binding portion thereof). Rather, the disclosure of the '846  
9 application suggests that a DR5 polypeptide binds a "DR5 ligand" (FFs 29 and  
10 30).

11 Ni's position is premised on classifying DR5 as a "putative TNF death  
12 receptor" based on the described similarity between the amino acid sequences of  
13 DR5 and three previously known TNF death receptors TNFR1, Fas and DR3 in  
14 the '846 application. According to Ni, TNFR1, Fas and DR3 were all known to  
15 induce apoptosis upon activation and, therefore, that same function should be  
16 imputed to DR5 by virtue of the described similarity in amino acid sequences  
17 between DR5 and the three TNF death receptors. Ni argues that the '846  
18 specification explicitly teaches that DR5 induces apoptosis and binds to a TNF  
19 ligand selected from a limited list including TRAIL. Ni further argues that, based  
20 on the doctrine of inherency, the '846 application need not expressly recite that  
21 DR5 binds TRAIL so long as the '846 application describes the subject matter of  
22 the Count. [Paper 30, p. 2, ¶ 3 and ¶ bridging pp. 9-10.]

- 1        35. Ni relies on the direct testimony of John C. Reed, M.D., Ph.D. (NX 2103)  
2        in support of its position.
- 3        36. Dr. Reed has been qualified as an expert to give opinions on the subjects  
4        of apoptosis and of the tumor necrosis family of ligands (TNFs) and  
5        receptors (TNFRs), including death receptors.
- 6        37. According to Dr. Reed, the deduced amino acid sequence of human DR5  
7        described in the '846 application has all the canonical (structural)  
8        features of a classic death receptor of the TNFR family, i.e., a leader  
9        peptide, conserved cysteine-rich domain(s), a transmembrane domain  
10       and a cytosolic domain containing a "death domain" (NX 2103, ¶ 28).
- 11       38. Further according to Dr. Reed, the death domain "is necessary and  
12       sufficient for apoptosis induction, at least when overexpressed in  
13       mammalian cells" (*id.*, ¶ 21).
- 14       39. Still further according to Dr. Reed, DR5 shares the highest degree of  
15       amino acid sequence identity with then known death receptor proteins  
16       human TNFR1, Fas and DR3 (*id.*, ¶ 29).
- 17       40. Dr. Reed states that the deduced amino acid sequence of the "death  
18       domain" region of the DR5 protein described in Ni's '846 application was  
19       approximately 21, 32 and 33 percent identical to the amino acid  
20       sequences of the death domains of Fas, TNFR1 and DR3, respectively,  
21       "using Lipman-Pearson Protein Alignment (with the following parameters:  
22       Ktuple 2; Gap Penalty 4; Gap Length Penalty 12)" (*id.*, ¶ 31).

- 1       41. Dr. Reed opines that a death domain amino acid sequence identity of  
2       approximately 21-33 percent is "significant" because Chinnaniyan (NX  
3       2058) reported that the death domain of DR3 was 47 and 23 percent  
4       identical to that of TNFR1 and Fas, respectively, while Marsters (NX  
5       2059) reported that the death domain of DR3 was 48 and 20 percent  
6       identical to that of TNFR1 and Fas, respectively (NX 2103, ¶ 31).
- 7       42. Chinnaiyan reported using MegAlign<sup>TM</sup> software to align the compared  
8       amino acid sequences (NX 2058, Fig. 1).
- 9       43. MegAlign<sup>TM</sup> software can create alignments between two or more  
10       sequences according to different methods, e.g., the clustal method or the  
11       Jotun Hein method (see e.g., U.S. Patent 6,277,568, col. 8, ll. 22-41).
- 12       44. Neither Chinnayian or Marsters reported the alignment program and  
13       parameters used to obtain their respective percent sequence identity  
14       scores.
- 15       45. Dr. Reed did not explain percent sequence identity scoring, e.g., how  
16       different alignment methods and parameters calculate percent sequence  
17       identity scores; how different alignment methods are compared  
18       (normalized to account for the use of different parameters, e.g.,  
19       sequence lengths, gaps, gap positions, etc.); the significance, if any, of  
20       comparing sequences within predicted structural features (e.g., a death  
21       domain or extracellular domain) versus over the entire primary amino  
22       acid sequence; standard error of the method(s) used; use of iteration,  
23       etc.

- 1           46. For example, according to Tartaglia,<sup>3</sup>  
2                   [i]t has been noted previously that the intracellular  
3                   domain of TNF-R1 shares a **weak homology (29%**  
4                   **identity over 45 amino acids)** with the intracellular  
5                   domain of Fas antigen. Upon further inspection of  
6                   these sequences, we noted that introduction of a 1  
7                   amino acid gap in the Fas sequence extended the  
8                   region of homology an additional 20 amino acids  
9                   (Figure 3). [NX 2067, p. 846, col. 2, ¶ 1, emphasis  
10                  added.]
- 11           47. Nonetheless, Dr. Reed believes that one of ordinary skill in the art would  
12                  have reasonably expected the putative death receptor DR5 of the '846  
13                  specification to have utilities similar to the known utilities of known death  
14                  receptors TNFR1, Fas and DR3 (NX 2103, ¶¶ 33-34).
- 15           48. According to Dr. Reed, "**the most reasonable conclusion to draw** from  
16                  Ni's March 17, 1997 application is that DR5 is expected, by persons of  
17                  ordinary skill in the art, to be a novel death receptor" and, therefore,  
18                  skilled artisans "**would have predicted** that activation of DR5 would  
19                  induce apoptosis" (NX 2103, ¶ 32, emphasis added).
- 20           49. Further according to Dr. Reed, activation (aggregation) of a death  
21                  receptor could be caused by (i) ligand binding to the death receptor, (ii)  
22                  antibody binding to the death receptor or (iii) overexpression of the death  
23                  receptor on the cell surface (id., ¶ 24).
- 24           50. Dr. Reed testified that  
25                  if one would want to determine which TNF ligand DR5  
26                  binds, Ni's March 17, 1997 application [i.e., the '846  
27                  application], in combination with what was known in  
28                  the art at the time, provides all of the necessary  
29                  information. For example, Ni's March 17, 1997

---

<sup>3</sup> Tartaglia et al. (Tartaglia), "A Novel Domain within the 55 kd TNF Receptor Signals Cell Death," Cell, Vol. 74, pp. 845-853 (10 September 1993) (NX 2067).

1 application states that **DR5 binds to a TNF-family**  
2 **ligand** (Exhibit 2042, pg. 4, ¶¶2-3; pg. 26, ¶1; pgs 28-  
3 29; pg. 31, ¶1, pg. 31, ¶1 [sic]), which would have  
4 been expected by a person of ordinary skill in the art  
5 in view of the literature that was available by March  
6 17, 1997. Additionally, Ni's March 17, 1997  
7 application specifically defines "a TNF family ligand"  
8 as a limited number of molecules, one of which is  
9 TRAIL. (Exhibit 2042, pg. 31, lines 4-9). The Ni  
10 March 17, 1997 application also teaches assays, such  
11 as cellular response **assays, that could be used to**  
12 **determine whether** TRAIL, or any other of the listed  
13 **TNF ligands, binds to DR5.** (Exhibit 2042, pg. 26,  
14 lines 12-26; pg. 27, line 21 through pg. 29, line 6).  
15 **Alternatively, as of March 17, 1997, it would have**  
16 **been routine** for a person of ordinary skill in the art to  
17 **have tested whether DR5 binds to the TNF-family**  
18 **ligands recited in Ni's May [sic] 17, 1997**  
19 **application, including TRAIL.** Thus, if one wanted to  
20 have determined whether DR5 bound to a TNF  
21 ligand, including TRAIL, the Ni March 17, 1997  
22 application, in combination with what was known in  
23 the art at the time, teaches all of the needed  
24 information. [NX 2103, ¶ 56, emphasis and bracketed  
25 text added.]

26 51. Dr. Reed notes that while most TNF family receptors have been shown  
27 experimentally to bind to specific TNF family ligands, some receptors "do  
28 not have known receptors to date, or a delay of many years occurred  
29 before the specific ligand was established" (NX 2103, ¶ 18).

30 52. According to the '846 specification, there are eleven known members of  
31 the TNF ligand family, i.e., TNF- $\alpha$ , lymphotoxin- $\alpha$  (LT- $\alpha$ , also known as  
32 TNF- $\beta$ ), LT- $\beta$  (found in complex heterotrimer LT- $\alpha$ 2- $\beta$ ), FasL, CD40,  
33 CD27, CD30, 4-1BB, OXO40, nerve growth factor (NGF) and TRAIL (NX  
34 2042, p. 1, ll. 21-25 and p. 31, ll. 6-9).

35 53. The '846 specification defines "TNF-family ligand" as

1 naturally occurring, recombinant, and synthetic  
 2 ligands that are capable of binding to a member of the  
 3 TNF receptor family and inducing the ligand/receptor  
 4 signaling pathway. Members of the TNF ligand family  
 5 include, but are not limited to, **DR5 ligands**, TRAIL,  
 6 TNF- $\alpha$ , lymphdotoxin- $\alpha$  (LT- $\alpha$ , also known as TNF- $\beta$ ),  
 7 LT- $\beta$  (found in complex heterotrimer LT- $\alpha$ 2- $\beta$ ), FasL,  
 8 CD40, CD 27, CD30, 4-1BB, OX40 and nerve growth  
 9 factor (NGF). [*Id.*, p. 31, ll. 4-9, emphasis added.]

10 54. Dr. Reed relies on Ni's later filed '201 application (NX 2056, Figure 6A)  
 11 and on a later published August 1997 article (NX 2031<sup>4</sup>) to support his  
 12 testimony that DR5 "necessarily" binds to TRAIL and "necessarily"  
 13 induces apoptosis (NX 2103, ¶ 57).

14 To be accorded benefit for the purpose of priority in an interference  
 15 proceeding "means Board recognition that a patent application provides a proper  
 16 constructive reduction to practice under 35 U.S.C. 102(g)(1)." 37 CFR § 41.201.  
 17 A constructive reduction to practice "means a described and enabled anticipation  
 18 under 35 U.S.C. 102(g)(1) in a patent application of the subject matter of a  
 19 count." *Id.* To fulfill the written description requirement, the patent specification  
 20 must describe an invention in sufficient detail that one skilled in the art can  
 21 clearly conclude that the inventor invented what is claimed. Lockwood v. Am.  
 22 Airlines, Inc., 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (Fed. Cir. 1997).  
 23 The specification "need not describe the claimed subject matter in exactly the  
 24 same terms as used in the claims; it must simply indicate to persons skilled in the  
 25 art that as of the [filing] date the applicant had invented what is now claimed."  
 26 Eiselstein v. Frank, 52 F.3d 1035, 1038, 34 USPQ2d 1467, 1470 (Fed. Cir. 1995)

---

<sup>4</sup> Guohua et al. (Guohua), "An Antagonist Decoy Receptor and a Death Domain-Containing Receptor for TRAIL," Science, Vol. 277, pp. 815-818 (8 August 1997). Three of the six coauthors are also Ni inventors.

1 (citations omitted). Furthermore, "the fact that a characteristic is a necessary  
2 feature or result of a prior-art embodiment (that is itself sufficiently described and  
3 enabled) is enough for inherent anticipation, even if that fact was unknown at the  
4 time of the prior invention." Toro Co. v. Deere & Co., 69 USPQ2d 1584, 1590  
5 (Fed. Cir. 2004) (citations omitted). Benefit for the purpose of priority focuses on  
6 the subject matter of a count and only requires a constructive reduction to  
7 practice of a single embodiment within the scope of the count. Falkner v. Inglis,  
8 463 F.3d 1376, 1379, 79 USPQ2d 1001, 1004 (Fed. Cir. 2006); Hunt v.  
9 Treppschuh, 523 F.2d 1386, 1389, 187 USPQ 426, 429 (CCPA 1975).<sup>5</sup>

10 Here, the subject matter of the count is directed to a functional protein, i.e., a  
11 purified TRAIL-R polypeptide having an amino acid sequence that is at least 90%  
12 identical to SEQ ID NO:2 of Rauch's involved '358 patent, wherein the  
13 polypeptide binds TRAIL (FF 11). Relying on the testimony of Dr. Reed, Ni  
14 argues that the similarity between the deduced amino acid sequence of DR5 and  
15 the known amino acid sequences of three TNF death receptor proteins, i.e.,  
16 TNFR1, Fas and DR3, as described in the '846 application is sufficient to  
17 characterize DR5 as a putative TNF death receptor protein and to predict that  
18 DR5 has utilities/functions similar to those of known death receptor proteins, e.g.,  
19 induction of apoptosis upon activation.

20 Neither the disclosure of the '846 application nor the testimony of Dr. Reed  
21 is as explicit as Ni argues. The '846 application suggests that DR5 is a putative  
22 TNF death receptor protein (FF 28). Dr. Reed testified that the most reasonable

---

<sup>5</sup> In contrast, benefit for the purpose of 35 U.S.C. § 120 and related statutes focuses on the subject matter of the claim and requires the application for which benefit is sought to describe and enable the entire scope of the claim.

1 conclusion a person of ordinary skill in the art would draw from the '846  
2 application is that DR5 "is expected ... to be a novel death receptor" (FF 48).  
3 The '846 specification does not describe preparing DR5 or a ligand binding  
4 portion thereof (e.g., expressing and purifying DR5 from the DNA of Figure 1).  
5 The '846 specification does not describe an activated (functional) DR5 or identify  
6 the TNF ligand which activates (binds to) DR5.

7       Since TRAIL was known to be capable of inducing apoptosis (FF 18),  
8 identifying TRAIL as the TNF ligand which bound to DR5 in the '846 specification  
9 would have been one way of describing DR5 as capable of inducing apoptosis.  
10 Dr. Reed testified that '846 application "states that DR5 binds to a TNF-family  
11 ligand" and that there were "assays, that could be used to determine whether  
12 TRAIL, or any other of the listed TNF ligands, binds to DR5" (FF 50). Dr. Reed  
13 further testified that "it would have been routine for one of ordinary skill in the art  
14 to have tested whether DR5 binds to the TNF-family ligands recited" in the '846  
15 application, "including TRAIL" (FF 50). Notably, the '846 specification  
16 enumerates "DR5 ligands" as separate and distinct ligands in its list of TNF  
17 ligands, including TRAIL (FF 53), implying that DR5 might bind to either a known  
18 TNF ligand, e.g., TRAIL, or an as yet unknown TNF ligand, i.e., a DR5 ligand, or  
19 another TNF ligand known to be capable of inducing another function, e.g., cell  
20 proliferation.

21       In short, there is neither explicit nor implicit disclosure in the '846  
22 application said to show that the DR5 polypeptide encoded by the DNA of Figure  
23 1 is a functional/bioactive protein. The cognate ligand for DR5 is not explicitly

1 identified in the '846 application, although it would have been routine for one of  
2 ordinary skill in the art to do so using known techniques, as testified to by Dr.  
3 Reed (FF 50). Moreover, there could be no explicit description of an activated  
4 DR5 based on antibody binding or overexpression in mammalian cells absent  
5 obtaining the DR5 polypeptide (e.g., by expressing the product of the DNA of  
6 Figure 1) against which to raise an antibody. Finally, a person skilled in the art  
7 could not have reasonably predicted the function(s) of DR5 based solely on the  
8 similarity between its deduced amino acid sequence as set forth in Figure 1 of  
9 the '846 application and the known amino acid sequences of TNFR1, Fas and  
10 DR3 in view of the state of the art when the '846 application was filed for the  
11 following reasons.

12 Genes encode proteins by providing a sequence of nucleic acids that is  
13 translated into a sequence of amino acids. Methods used to identify novel genes  
14 are classified into two types, i.e., homology based or non-homology based. In  
15 homology based methods, for example, clones from a cDNA library are cloned  
16 and analyzed (sequenced). The resultant nucleotide sequences and/or deduced  
17 amino acid sequences are checked against databases for similarity (homology)  
18 to previously characterized sequences on the theory that molecules with similar  
19 sequences would be expected to perform similar functions. However, one of the  
20 difficulties in identifying a functional protein is that function depends not only on  
21 the amino acid sequence of the protein, but also on other factors, e.g., the three-  
22 dimensional structure of the protein.

1           In order for a protein to function properly its amino acid sequence (primary  
2   structure) must fold itself up into a complex three-dimensional shape which  
3   allows for molecular recognition. Molecular recognition often involves only a  
4   small number of key amino acid residues on the functional surfaces of interacting  
5   molecules. These residues are dispersed in diverse regions of the primary  
6   amino acid sequence due to the complex structural organization of the protein.  
7   There are multiple levels to the structural organization of a protein. The *primary*  
8   *structure* of a protein refers to the linear arrangement of amino acid residues  
9   along a polypeptide chain. *Secondary structures* form through interactions  
10   between amino acids typically found near each other in the peptide chain which  
11   fold parts of the chain into regular structures, e.g.,  $\alpha$  helices and  $\beta$  sheets.  
12   *Tertiary structure* folds both the secondary structures and the regions between  
13   them into compact three-dimensional shapes in an energetically favourable way.  
14   *Quaternary structure* refers to the organization of several polypeptide chains into  
15   a single protein molecule, e.g., hemoglobin is a tetramer. Consequently, amino  
16   acid residues rather near to each other in a protein's primary structure may be  
17   rather distant in the protein's ultimate quaternary structure. [See generally,  
18   MOLECULAR CELL BIOLOGY ("MCB"), second edition, Darnell et al., W.H.  
19   Freeman and Company, New York, NY (1990), pp. 44-48 (copy enclosed).]  
20           For example, an enzyme is a protein that catalyzes a biochemical  
21   reaction. The function of an enzyme relies on the structure of its "active site," a  
22   specific cavity-like region on the surface of the three-dimensional enzyme which  
23   allows a spatial fit (molecular recognition) between the enzyme and its substrate

1 (reactant in the reaction being catalyzed). The active site contains key amino  
2 acids that bind the substrate and are involved in the reaction catalyzed by the  
3 enzyme. These key amino acids are brought into proximity (into the active site)  
4 by protein folding. [See generally, MICROBIOLOGY: An Introduction, Tortora et  
5 al., The Benjamin/Cummings Publishing Company, Inc., Menlo Park, California  
6 (1982), pp. 111-112, copy enclosed; MCB, pp. 55-65, copy enclosed.]

7 On the other hand, mutations that cause human disease often disrupt  
8 protein structure, thereby altering or abolishing normal protein function. For  
9 example, sickle cell anemia occurs in humans that are homozygous for a  $\beta$ -  
10 hemoglobin gene that differs from the normal adult hemoglobin gene by a single  
11 base pair, resulting in a change in a single amino acid from glutamate to valine in  
12 position 5. This substitution is on the surface of the abnormal hemoglobin (Hb S)  
13 and changes the electrostatic charge on the surface of Hb S. When oxygen is  
14 removed from Hb S, the protein polymerizes into rigid crystals that deform a  
15 sickle cell patient's red blood cells. Thus, although normal hemoglobin and Hb S  
16 have virtually identical primary amino acid sequences, a single amino acid  
17 change in Hb S alters its quaternary structure and results in abnormal protein  
18 function. [See generally, CLINICAL DIAGNOSIS AND MANAGEMENT BY  
19 LABORATORY METHODS, sixteenth edition, J.B. Henry ed., W.B. Saunders  
20 Company, Philadelphia (1979), Vol. I, p. 992, copy enclosed.]

21 Therefore, "[s]equence comparison can indicate whether an RNA or  
22 protein molecule or region of DNA is already known (identity) or has some  
23 degree of similarity to a known sequence" (MOLECULAR BIOLOGY AND

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 22  
Paper 101

1 BIOTECHNOLOGY, R. Myers, ed., VCH Publishers, Inc., New York, NY (1995),  
2 p. 860, c. 1, ¶ 1, copy enclosed). However, since "[t]he function of nucleic acids  
3 and proteins depend on their structure and involves complex interactions in three  
4 dimensions",

5 [i]t is not presently understood whether it is possible,  
6 in general, to derive structure from sequence.  
7 Sequence alone is therefore often inadequate to  
8 determine function. Predictions made from sequence  
9 analysis need to be experimentally tested.  
10 Nonetheless, computer analysis of sequences is  
11 valuable in suggesting the most useful experiments to  
12 perform. [*Id.*, p. 860, c. 1, ¶ 2.]

13 Indeed, the difficulties in predicting the structure and function of a protein from  
14 just its amino acid sequence (primary structure) are so well known in the art that  
15 the ability to characterize the function and structure of a protein from its amino  
16 acid sequence has been called the "Holy Grail" of molecular biology (RX 1061,<sup>6</sup>  
17 p. 511, c. 2, ¶ 1 to p. 512, c. 1, ¶ 1).

18 55. Genchong Cheng, Ph.D., is a witness for Rauch and has been qualified  
19 as an expert to give opinions on the subjects of signal transduction and  
20 gene expression networks through the TNFR, Toll-like receptor (TLR)  
21 and Nod receptor families during immune responses.

22 56. Dr. Cheng testified that

23 [s]equence homology to other death domain-  
24 containing TNF receptors may be sufficient to  
25 convince one of ordinary skill in the art that a novel  
26 protein is a TNFR family member. However,  
27 sequence homology alone is not sufficient to support  
28 an assertion that a novel TNFR family member  
29 protein will induce specific biological activities such as

---

<sup>6</sup> Pawlowski et al., "From fold to function predictions: an apoptosis regulator protein BID,"  
Computers and Chemistry, Vol. 24, pp. 511-517 (2000) (RX 1061).

1 apoptosis. Without additional data regarding the  
2 activity of a TNFR family member, such as, for  
3 example, the identity of the ligand with a known  
4 function (such as TRAIL) to which the receptor binds,  
5 one of ordinary skill in the art cannot reasonably  
6 predict the function of the TNFR family member. [RX  
7 1039, ¶ 17.]

8 Ni's own witness, Dr. Reed, did not testify that the specification and figures  
9 of the '846 application would have reasonably conveyed to a skilled artisan that a  
10 DR5 having the deduced amino acid sequence shown in Figure 1 is in fact a  
11 functional death receptor protein based solely on its amino acid sequence  
12 (primary structure). Dr. Reed did not testify that the skilled artisan would have  
13 understood the '846 application to describe a functional death receptor. Rather,  
14 Dr. Reed testified to "the most reasonable" (not the necessary and always)  
15 conclusion that one of ordinary skill in the art would have drawn from the  
16 disclosure of the '846 application (FF 48).

17 Dr. Reed also testified that there was a "significant" percent sequence  
18 identity between the deduced amino acid sequence of DR5's death domain and  
19 the amino acid sequence of the death domains of TNFR1, Fas and DR3 (FFs 40  
20 and 41). However, Dr. Reed's testimony in this regard is entitled to little, if any,  
21 weight because Dr. Reed did not provide a sufficient basis for his opinion. Dr.  
22 Reed did not explain how percent sequence identity scores were obtained,  
23 identify what alignment methods and parameters were used by the "references"  
24 (Chinnaiyan (NX 2058)<sup>7</sup> and Marsters (NX 2059)<sup>8</sup>), explain how percent identify

---

<sup>7</sup> Chinnaiyan et al. (Chinnaiyan), "Signal Transduction by DR3, a Death Domain-Containing Receptor Related to TNFR-1 and CD95," Science, Vol. 274, pp. 990-992 (8 November 1996) (NX 2058).

1 scores based on different alignment methods and parameters relate to each  
2 other, what standard of error was typically found, whether iteration was  
3 necessary to obtain a statistically valid result, etc. 37 CFR § 41.158; Standing  
4 Order ¶ 24. Further, as illustrated by the discussion of Hb S above, even very  
5 small differences between protein variants with highly similar amino acid  
6 sequences can produce significant differences in function.

7 Therefore, in view of the state of the art at the time the '846 application  
8 was filed and the testimony of both Drs. Reed and Cheng, we find that the '846  
9 application does not describe an enabled embodiment (a functional DR5 having  
10 the deduced amino acid sequence shown in Figure 1) within the scope of Count  
11 1. The '846 application does describe a DR5 which may be preliminarily  
12 classified as a TNF death receptor protein based upon its deduced amino acid  
13 sequence. However, given the unpredictability of determining function from  
14 structure, a skilled artisan would have had to carry out further research to identify  
15 the function(s) of DR5 having the deduced amino acid sequence set forth in  
16 Figure 1.

17 Anticipation is a question of fact, not a conclusion of law, no matter how  
18 reasonable that conclusion may appear to be. Putative assignment to a protein  
19 (sub)family does not assess the actual biological function/utility of a nucleic acid  
20 sequence and its encoded protein product. Ni has failed to establish that the  
21 '846 application describes a functional death receptor protein within the scope of  
22 the count based solely on the disclosure of a deduced amino acid sequence.

---

<sup>8</sup> Marsters et al. (Marsters), "Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF- $\kappa$ B," Current Biology, Vol. 6, No. 12, pp. 1669-1676 (1996) (NX 2059).

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 25  
Paper 101

1 Brenner v. Manson, 383 U.S. 519, 532, 148 USPQ 689, 694 (1966) ("the  
2 presumption that adjacent homologues have the same utility has been  
3 challenged in the steroid field because of 'greater known unpredictability of  
4 compounds in that field.'").

5 Ni also argues that the DR5 protein of the '846 application inherently binds  
6 TRAIL and that the '846 specification explicitly teaches that DR5 binds a TNF  
7 ligand selected from a limited list which includes TRAIL (Paper 30, p. 2, ¶ 3).  
8 However, before considering whether a limitation is an inherent characteristic of  
9 an embodiment within the scope of a count, that embodiment must itself be  
10 sufficiently described and enabled. Toro, 69 USPQ2d at 1590. Thus, this  
11 argument fails because Ni has not established that the '846 application describes  
12 an enabled embodiment within the scope of the count for the reasons above.  
13 Secondly, arguing that DR5 binds a TNF ligand from a limited list which includes  
14 TRAIL is also unpersuasive because the so-called "limited" list appears to cover  
15 all the known and unknown ligands of the TNF family, i.e., the list enumerates the  
16 eleven then known TNF ligands and then adds a catch-all "DR5 ligands,"  
17 seemingly in the event DR5 did not bind any of the then known TNF ligands.  
18 Neither the disclosure of the '846 application nor the testimony of Dr. Reed  
19 suggests that DR5 necessarily and always binds TRAIL or that DR5 binds a  
20 specific ligand from the "limited" subset of TNF ligands. Moreover, Ni's reliance  
21 on case law is misplaced.

22 Ni argues that  
23 even without express appreciation of a limitation  
24 recited in a count, disclosure in a priority application  
25 of an embodiment which is later shown to *inherently*

1 possess a characteristic satisfying that limitation is  
2 sufficient to establish constructive reduction to  
3 practice. See e.g., *Silvestri v. Grant*, 496 F.2d 593,  
4 599, 181 U.S.P.Q. 706, 710 (CCPA 1974) ("The  
5 invention is not the language of the count but the  
6 subject matter defined thereby."); See also *Hudziak v.*  
7 *Ring*, 2005 Pat. App. LEXIS 26 (Bd. Pat. App. Intf.,  
8 Sept. 2005) (confirming that a party's priority  
9 applications, which disclosed an antibody but did not  
10 state the antibody bound to a particular receptor  
11 protein (HER2) as recited in the count, were  
12 nonetheless constructive reductions to practice  
13 because subsequent evidence showed that the  
14 antibody bound HER2.) [Paper 30, p. 8, ¶ 1, original  
15 emphasis.]

16 Neither Silvestri nor Hudziak are on point. Silvestri has been discussed  
17 above (§III. Ni Substantive Motion 1). In Silvestri, the court held that the  
18 evidence established that Silvestri had prepared a new form of ampicillin,  
19 recognized and appreciated the existence of the new form of ampicillin, and that  
20 the new form of ampicillin had utility. Id., 496 F.2d at 598-601, 181 USPQ at  
21 709-712. The court acknowledged that the ampicillin of the count required a  
22 molecular weight of about 349 and greater storage stability than the previously  
23 known form of ampicillin. However, the court thought these were inherent  
24 properties of the new form of ampicillin that Silvestri was said to have obtained,  
25 recognized and described. Id., 496 F.2d at 599, 181 USPQ at 709. The court  
26 noted in Silvestri that the reduction to practice test does not require in haec verba  
27 appreciation of each of the limitations of the count:

28 This standard does not require that Silvestri establish  
29 that he recognized the invention in the same terms as  
30 those recited in the count. The invention is not the  
31 language of the count but the subject matter thereby  
32 defined. Silvestri must establish that he recognized  
33 and appreciated as a new form, a compound

1 corresponding to the compound defined by the count.  
2 Id., 496 F.2d at 599, 181 USPQ at 710

3 Here, the compound of the count is a functional protein which has at least  
4 90% identity to a defined amino acid sequence and binds TRAIL. Thus, it is  
5 necessary to consider whether the '846 application describes properties/uses of  
6 DR5. The '846 application only speculates that DR5 has desired properties, e.g.,  
7 inducing apoptosis upon activation. Ni is not in the same position as Silvestri  
8 whose application was said to have described obtaining an ampicillin compound,  
9 to have recognized it as a new form of ampicillin and to have described certain  
10 properties of the compound. Ni's '846 application describes a precursor to an  
11 encoded protein and speculates on the nature and properties of that protein.  
12 Therefore, Silvestri is not on point.

13 Similarly, in Hudziak v. Ring, 80 USPQ2d 1018, 1019 (Bd. Pat. App. & Int.  
14 2005), the count was directed to a monoclonal antibody that bound human  
15 epidermal growth factor receptor 2 (HER2). A panel of the Board decided that  
16 Chiron's (Ring's real party-in-interest) 1984 application disclosed an embodiment  
17 within the count, i.e., a murine monoclonal antibody designated 454C11. Id. The  
18 panel noted that the 1984 application (06/577,976) stated that hybridomas which  
19 produced 454C11 were deposited with the ATCC and that evidence submitted by  
20 Chiron established that 454C11 bound HER1. Id. at 1020-21.

21 57. The panel also noted in its decision (Paper 258, p. 129) that "Table 3 of  
22 the 1984 application reports the binding of antibodies to breast cancer  
23 cell lines and indicates that 454C11 binds to SKBR3 cells, which are now  
24 known to express HER2. (CX 1081, p. 3)."

1        Thus, in Hudziak, Chiron was said to have actually prepared an embodiment  
2        within the count, monoclonal antibody 454C11, and to have described it as a new  
3        protein and to have appreciated one of its properties/functions, i.e., that it bound  
4        to breast cancer cells. Ni's '846 application describes a precursor to an encoded  
5        protein and speculates on the nature and properties of that protein. Therefore,  
6        Hudziak is not on point.

7        Since Ni has failed to establish that the '846 application describes an  
8        enabled compound (functional DR5 protein) within the scope of the count, we do  
9        not reach the issue of what the inherent characteristics of that protein are. In  
10       both Silvestri and Hudziak, the application was said to specifically describe  
11       compounds that were recognized as novel and as having certain properties.  
12       These described and characterized compounds were later found to have other  
13       properties required by the count. Here, the '846 application does not describe  
14       and characterize a functional protein. Ni's application only speculates on the  
15       nature and properties of the protein encoded by the DNA of Figure 1 and that  
16       speculation is insufficient to show possession of an enabled embodiment within  
17       the count (which may later be found to have other properties required by the  
18       count).

19       Based on the foregoing, Ni is not entitled to benefit for the purpose of  
20       priority of the filing date of the '846 application as to Count 1.

21       In conclusion, Ni substantive motion 2 is **granted-in-part, denied-in-part**  
22       and **dismissed-in-part**.

23

1           **VI.           Rauch Substantive Motion 3**

2           Pursuant to 37 CFR § 41.121(a)(1)(iii) and the Order issued 29 November  
3           2005 (Paper 26), Rauch moves for judgment that Ni's '842 application claims 35,  
4           36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-109, 111-116, 127-133, 168-  
5           178 and 180-203 ("Ni's involved claims") are unpatentable under 35 U.S.C. §  
6           102(a) and/or (e) as clearly anticipated by one or more of U.S. Patent 6,642,358  
7           ("the '358 patent," RX 1042), U.S. Patent 6,072,047 ("the '047 patent," RX 1048),  
8           U.S. Patent 6,569,642 ("the '642 patent," RX 1046) and WO 98/35986 ("WO  
9           '986," RX 1032) (collectively, "the Rauch references") (Paper 36, p. 25). Ni  
10          opposes (Paper 49); Rauch replies (Paper 66).

11          58. According to the '358 patent, it issued 4 November 2003 based on  
12          application 09/578,392, filed 25 May 2000, which is a divisional of  
13          application 08/883,036, filed 26 June 1997, which is a continuation-in-  
14          part of application 08/869,852, filed 4 June 1997, which is a continuation-  
15          in-part of application 08/829,536, filed 28 March 1997, which is a  
16          continuation-in-part of application 08/815,255, filed 12 March 1997, which  
17          is a continuation-in-part of application 08/799,861, filed 13 February 1997  
18          (RX 1042, title page).

19          59. According to the '047 patent, it issued 6 June 2000 based on application  
20          08/883,036, filed 26 June 1997, which is a continuation-in-part of  
21          application 08/869,852, filed 4 June 1997, which is a continuation-in-part  
22          of application 08/829,536, filed 28 March 1997, which is a continuation-  
23          in-part of application 08/815,255, filed 12 March 1997, which is a

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 30  
Paper 101

1 continuation-in-part of application 08/799,861, filed 13 February 1997  
2 (RX 1048, title page).

3 60. According to the '642 patent, it issued 27 May 2003 based on application  
4 09/536,201, filed 27 March 2000, which is a continuation-in-part of  
5 application 08/883,036, filed 26 June 1997, which is a continuation-in-  
6 part of application 08/869,852, filed 4 June 1997, which is a continuation-  
7 in-part of application 08/829,536, filed 28 March 1997, which is a  
8 continuation-in-part of application 08/815,255, filed 12 March 1997, which  
9 is a continuation-in-part of application 08/799,861, filed 13 February 1997  
10 (RX 1046, title page).

11 61. WO '968 published 20 August 1998, based on international application  
12 PCT/US98/02239, filed 11 February 1998 (RX 1032, title page).

13 According to the relevant paragraphs of 35 U.S.C. § 102:

14 [a] person shall be entitled to a patent unless--

15 (a) the invention was known or used by others  
16 in this country, or patented or described in a printed  
17 publication in this or a foreign country before the  
18 invention thereof by the applicant for patent, or

19 \* \* \* \* \*

20 (e) the invention was described in (1) an  
21 application for a patent, published under section  
22 122(b), by another filed in the United States before  
23 the invention by the applicant for patent or (2) a  
24 patent granted on an application for patent by another  
25 filed in the United States before the invention by the  
26 applicant for patent, except that an international  
27 application filed under the treaty defined in section  
28 351(a) shall have the effects for the purposes of this  
29 subsection of an application filed in the United States  
30 only if the international application designated the

Letter Brief  
Ex. C  
D-M

1 United States and was published under Article 21(2)  
2 of such treaty in the English language, or

3 \* \* \* \* \*

4 References based on international applications that were filed prior to 29  
5 November 2000 are subject to the former version of 35 U.S.C. § 102(e),<sup>9</sup> i.e.,

6 [a] person shall be entitled to a patent unless --

7 (e) the invention was described in a patent  
8 granted on an application for patent by another filed in  
9 the United States before the invention thereof by the  
10 applicant for patent, or on an international application  
11 by another who has fulfilled the requirements of  
12 paragraphs (1), (2), and (4) of section 371(c) of this  
13 title before the invention thereof by the applicant for  
14 patent.

15 A prima facie case is made out under § 102(a) if, within a year of the filing  
16 date, the invention, or an obvious variant thereof, is described in a "printed  
17 publication" whose authorship differs from the inventive entity unless it is stated  
18 within the publication itself that the publication is describing the applicant's work.  
19 In re Katz, 687 F.2d 450, 215 USPQ 14 (CCPA 1982).

20 62. None of the Rauch references issued or published prior to the 17 March  
21 1998 filing date of the Ni claims at issue.<sup>10</sup>

22 63. None of the Rauch references qualify as prior art under § 102(a) vis-à-vis  
23 the Ni claims at issue.

24 Therefore, to the extent Rauch substantive motion 3 seeks a judgment that  
25 any of the Ni claims at issue are unpatentable under § 102(a) as anticipated by

---

<sup>9</sup> Pursuant to § 13205 of Pub. L. 107-273.

<sup>10</sup> Rauch has not argued prior knowledge or use of the subject matter of any of the Ni claims at issue.

1 any of the Rauch references, the motion is **denied**. We now consider whether  
2 any of the Rauch references qualify as prior art under § 102(e).

3 WO '986 is based on an international application filed prior to 29 November  
4 2000 (FF 61). Therefore, it must satisfy the requirements of the then applicable  
5 former § 102(e) in order to qualify as prior art. Rauch has neither argued nor  
6 shown that WO '986 satisfies the requirements of the applicable § 102(e) (see  
7 Paper 36, p. 22, ¶ 2). Thus, Rauch has not established that WO '986 qualifies as  
8 prior art under the applicable § 102(e) vis-à-vis the Ni claims at issue.

9 Consequently, to the extent Rauch substantive motion 3 seeks a judgment that  
10 any of the Ni claims at issue are unpatentable under § 102(e) as anticipated by  
11 WO '986, the motion is **denied**.

12 As indicated above (FFs 58-60), the '358, '047 and '642 patents are related.  
13 The '047 patent issued based on application 08/833,036 and the '358 and '642  
14 patents issued based on an application identified as a divisional or a  
15 continuation-in-part, respectively, of application 08/833,036, filed on 26 June  
16 1997. The filing date of the 08/833,036 application is prior to the 17 March 1998  
17 filing date of Ni's involved claims and prima facie qualifies as prior art under  
18 § 102(e) against the Ni claims at issue. It is not necessary to consider whether  
19 the Ni claims at issue are anticipated by the '358 and '642 patents, if the Ni claims  
20 at issue are anticipated by the '047 patent.

21 Claim chart appendix I attached to Rauch substantive motion 3 (Paper 36,  
22 beginning at p. 243) correlates the disclosure of the '047 patent to each of the  
23 limitations of each of the Ni claims at issue. Therefore, Rauch substantive

1 motion 3, when considered in light of the evidence relied upon in support of the  
2 motion, establishes a sufficient basis for holding the Ni claims at issue prima  
3 facie unpatentable under § 102(e) as anticipated by the '047 patent.

4 As noted by Rauch in its reply (Paper 66, p. 6, ¶ 1), Ni does not contest that  
5 the '047 patent describes the subject matter of its claims at issue. Rather, Ni  
6 argues that the '047 patent does not qualify as prior art because Ni's '583  
7 application claims are said to be entitled to benefit of the 17 March 1997 filing  
8 date of Ni's '846 application (Paper 49, p. 2, ¶ 2; ¶ bridging pp. 24-25; Appendix  
9 E).<sup>11</sup> Rauch maintains that Ni cannot obtain benefit of the filing date of its '846  
10 application due to a lack of utility (Paper 36, p. 22, ¶ 3 through p. 24, ¶ 1).

11 As stated in In re Fisher, 421 F.3d 1365, 1378, 76 USPQ2d 1225, 1235  
12 (Fed. Cir. 2005),

13 [i]t is well established that the enablement  
14 requirement of § 112 incorporates the utility  
15 requirement of § 101. The how to use prong of  
16 section 112 incorporates as a matter of law the  
17 requirement of 35 U.S.C. § 101 that the specification  
18 disclose as a matter of fact a practical utility for the  
19 invention. If the application fails as a matter of fact to  
20 satisfy 35 U.S.C. § 101, then the application also fails  
21 as a matter of law to enable one of ordinary skill in the  
22 art to use the invention under 35 U.S.C. § 112.

23 The dispositive question here is whether the Ni claims at issue are entitled to  
24 benefit of the 17 March 1997 filing date of Ni's '846 provisional application,  
25 thereby, antedating the 26 June 1997 filing date of the '047 patent. Benefit for  
26 purposes of antedating prior art, in this case, benefit under 35 U.S.C. § 119(e), is

---

<sup>11</sup> We need not consider whether Ni's '842 application claims are entitled to § 119(e) benefit of the 17 March 1998 filing date of Ni's '583 application or the 29 July 1997 filing date of Ni's '021 application because both of these two filing dates are after the 26 June 1997 filing date of the 08/833,036 application which issued as Rauch's '047 patent.

1 different from benefit for the purpose of priority. To obtain benefit of the filing  
2 date of a provisional application under § 119(e), the provisional application must,  
3 in relevant part, satisfy the description and enablement requirements of § 112,  
4 first paragraph, for the full scope of the claimed subject matter for which benefit is  
5 being sought. Ni and Rauch disagree as to whether the disclosure of Ni's '846  
6 provisional application satisfies the description and enablement requirements of  
7 § 112, first paragraph, as to the full scope of the subject matter of the Ni claims at  
8 issue.

9 Ni cites to specific disclosures in its '846 application said to describe every  
10 element of its claims at issue (Appendix E attached to Paper 49). Ni argues that  
11 the '846 application discloses that DR5 polypeptides are useful (a) to make anti-  
12 DR5 antibodies for treating or diagnosing diseases associated with apoptosis or  
13 (b) as antagonists of DR5 signaling (Paper 49, p. 7, ¶¶ 1-2).

14 64. Dr. Reed, testifying for Ni, stated that the technology necessary to  
15 achieve these functions was within routine skill in the art, e.g., a skilled  
16 artisan would know how to express and purify a protein (e.g., DR5) from  
17 cDNA (e.g., DNA of Figure 1 in the '846 application), how to produce  
18 antibodies that bind to a desired protein (e.g., DR5), etc. (NX 2103, ¶¶  
19 35-46).

20 65. Dr. Reed further testified that the uses for DR5 described in the '846  
21 application would have been believable to one of ordinary skill in the art  
22 because the asserted uses had previously been shown to be recognized

1 uses of TNF death receptors TNFR1, Fas and/or DR3 (NX 2103, ¶¶ 33-  
2 34 and 47-52).

3 Essentially, Dr. Reed's testimony as to the utility/enablement of DR5 is  
4 based on the assumption that the DR5 described in the '846 application is a  
5 functional TNF death receptor protein and, therefore, what was known about the  
6 use of other TNF death receptors was directly applicable to DR5 (see e.g., NX  
7 2103, ¶¶ 49 and 50 ("[b]ased on precedent from prior work in the field of TNF-  
8 family receptors" and "[b]ased on precedent from the literature where agonistic  
9 and antagonistic antibodies to other TNF-family receptors had been produced  
10 and characterized," respectively)). According to Ni, Dr. Reed "has testified  
11 unequivocally that 'you can reasonably make a prediction based on homology  
12 alone' and by analyzing 'the particular subfamily of proteins to which DR5  
13 belongs, *i.e.*, death receptors", "the most reasonable conclusion to draw from Ni's  
14 March 17, 1997 application is that DR5 is expected, by persons of ordinary skill  
15 in the art to be a novel death receptor [and that] a person of ordinary skill in the  
16 art would have predicted that activation of DR5 would induce apoptosis" (Paper  
17 49, p. 10, ¶ 1, citations omitted). The disclosure cited by Ni in its Appendix I is no  
18 more specific than Dr. Reed's testimony. For example, in the third paragraph of  
19 the third column on page 1 of Appendix I, Ni points to p. 6, lines 25-34 of the '846  
20 application as disclosing that "[t]he homology DR5 shows to other death domain  
21 containing receptors strongly indicates that DR5 is also a death domain  
22 containing receptor with the ability to induce apoptosis." Thus, according to Ni,  
23 Dr. Reed properly focused on the subset of known death receptors and the

1 "single" function that unites them, i.e., their ability to induce apoptosis (Paper 49,  
2 pp. 9-10).

3 Rauch, on the other hand, argues that sequence homology alone is  
4 insufficient to establish that the DR5 polypeptide disclosed in the '846 application  
5 is in fact a TNF family death domain receptor. According to Rauch, unless the  
6 disclosure of the '846 application shows DR5 to be an actual TNF family member  
7 receptor, e.g., by identification of a known TNF ligand as its cognate ligand or by  
8 specific experimental data showing that DR5 induces a TNFR-mediate biological  
9 activity, e.g., apoptosis, inflammatory response, etc., the '846 application fails to  
10 disclose a specific, substantial and credible utility for the DR5 and, therefore, for  
11 the Ni claims at issue (Paper 36, ¶ bridging pp. 23-24).

12 66. Dr. Cheng testified for Rauch that Ni's '846 application discloses

13 the DNA and amino acid sequence of the 411 amino  
14 acid isoform of TR-2, which they refer to as DR5.  
15 DR5 was identified based on sequence homology to  
16 other death domain-containing members of the TNFR  
17 family, including TNFR-1, DR3, and Fas ('846  
18 Provisional, page 5, lines 21-24). The applicants  
19 assert that agonists to DR5 can be used to increase  
20 apoptosis, while antagonists to DR5 can be used to  
21 inhibit apoptosis. This assertion is based entirely on  
22 sequence homology between DR5 and death domain-  
23 containing receptors TNFR-1, DR3, and Fas.  
24 However, the '846 Provisional does not identify a  
25 ligand for DR5, and contains no experimental data  
26 regarding DR5 function.

27 Sequence homology to other death domain-  
28 containing TNF receptors may be sufficient to  
29 convince one of ordinary skill in the art that a novel  
30 protein is a TNFR family member. However,  
31 sequence homology alone is not sufficient to support  
32 an assertion that a novel TNFR family member  
33 protein will induce specific biological activities such as  
34 apoptosis. Without additional data regarding the

1 activity of a TNFR family member, such as, for  
2 example, the identity of the ligand with a known  
3 function (such as TRAIL) to which it binds, one of  
4 ordinary skill in the art cannot reasonably predict the  
5 function of the TNFR family member. This is because  
6 TNFR family members are involved in complex signal  
7 transduction pathways which can affect a wide  
8 spectrum of biological activities including apoptosis,  
9 inflammatory response, cell proliferation, cell survival  
10 and other activities. The binding of certain TNFR  
11 family members by their corresponding ligands can  
12 lead to activation of multiple signal transduction  
13 pathways. As stated above, the '846 Provisional  
14 contains no data regarding the ligand for DR5, nor  
15 does it disclose experimental data of its function.  
16 Without knowing more information about the activity  
17 of DR5, such as for example its specificity for a ligand  
18 with a known function, one of ordinary skill in the art  
19 could not reasonably predict the function of the TNFR  
20 family member protein. [RX 1039, ¶¶ 16-17.]

21 For essentially the reasons set forth in our analysis in "§VI. Ni Substantive  
22 Motion 2" above, we credit the testimony of Dr. Cheng over that of Dr. Reed. In  
23 short, one of ordinary skill in the art might classify DR5 as disclosed in Ni's '846  
24 application as a possible TNF death receptor protein based on the similarity  
25 between its deduced amino acid sequence and the known amino acid sequences  
26 of TNF death receptor proteins TNFR1, Fas and DR3. However, given the  
27 unpredictability of determining function from structure (the "Holy Grail" of  
28 molecular biology), a skilled artisan would have had to carry further research to  
29 identify the function(s) of a DR5 polypeptide having the deduced amino acid  
30 sequence set forth in Figure 1 of the '846 application. Thus, the disclosure of the  
31 '846 application fails to satisfy the "how-to-use" requirement of § 112, first  
32 paragraph, as to the subject matter of the Ni claims at issue. The Ni claims at  
33 issue are, therefore, not entitled to § 119(e) benefit of the filing date of Ni's '846

1 application and Rauch's '047 patent still qualifies as prior art under § 102(e).  
2 Therefore, Ni claims 35, 36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-109,  
3 111-116, 127-133, 168-178 and 180-203 of Ni's '842 application (the Ni claims at  
4 issue) are unpatentable under 35 U.S.C. § 102(e) as anticipated by U.S. Patent  
5 6,072,047. It is not necessary to our decision to consider whether the Ni claims  
6 at issue are also anticipated by either the '358 or '642 patent.

7 In its opposition, Ni also argues that Rauch substantive motion 3 should  
8 be denied on procedural grounds because it does not seek judgment that all of  
9 Ni's involved claims are unpatentable and, therefore, is not a proper threshold  
10 motion (Paper 49, p. 13, ¶ 2 - p. 14, ¶ 1). Rauch substantive motion 3 is an  
11 ordinary attack on patentability. Ni has not provided any basis requiring a motion  
12 for unpatentability to attack all of a party's involved claims and we know of none.  
13 Therefore, this argument is without merit.

14 Based on the foregoing, Rauch substantive motion 3 is **granted only to**  
15 **the extent** that Ni claims 35, 36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-  
16 109, 111-116, 127-133, 168-178 and 180-203 are unpatentable under 35 U.S.C.  
17 § 102(e) as anticipated by U.S. Patent 6,072,047.

18 **VII. Rauch Substantive Motion 2**

19 Pursuant to 37 CFR § 41.121(a)(1)(i), Rauch moves to redefine the scope  
20 of the interference by designating Ni claims 46, 55, 63, 64, 110 and 118 of the  
21 '842 application as corresponding to Count 1 (Paper 35). Ni opposes (Paper 48);  
22 Rauch replies (Paper 65).

23 67. Ni '842 application claim 46, written in independent form, reads

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 39  
Paper 101

1 An isolated polypeptide comprising an amino acid  
2 sequence at least 95% identical to amino acids -50 to  
3 360 of SEQ ID NO:2, wherein said polypeptide  
4 induces apoptosis.

5 68. Ni '842 application claim 55, written in independent form, reads:

6 An isolated polypeptide comprising an amino acid  
7 sequence at least 95% identical to amino acids -51 to  
8 360 of SEQ ID NO:2, wherein said polypeptide  
9 induces apoptosis.

10 69. Ni '842 application claim 63, written in independent form, reads:

11 An isolated polypeptide comprising amino acids -50 to  
12 360 of SEQ ID NO:2.

13 70. Ni '842 application claim 64, written in independent form, reads:

14 An isolated polypeptide comprising amino acids -51 to  
15 360 of SEQ ID NO:2.

16 71. Ni '842 application claim 110, written in independent form, reads:

17 An isolated polypeptide comprising an amino acid  
18 sequence at least 95% identical to the full length  
19 amino acid sequence encoded by the cDNA clone in  
20 ATCC Deposit No. 97920, wherein said polypeptide  
21 induces apoptosis.

22 72. Ni '842 application claim 118, written in independent form, reads:

23 An isolated polypeptide comprising the full length  
24 amino acid sequence encoded by the cDNA clone in  
25 ATCC Deposit No. 97920.

26 73. SEQ ID NO:2 of Rauch's involved '358 patent contains 440 amino acid  
27 residues.

28 74. Amino acid residues 1 to 440 of Rauch '358 patent are identical to amino  
29 acid residues -51 to 360 of SEQ ID NO:2 of Ni's 842 application except  
30 for the inclusion of additional amino acid residues 185 to 213 in SEQ ID  
31 NO: 2 of Rauch's '358 patent (RX 1040, pp. 24-25 and RX 1042, ccs. 33-  
32 35).

1       75. According to Ni's '842 specification, the polypeptide encoded by the  
2       cDNA clone in ATCC Deposit No. 97920 has the amino acid sequence  
3       recited in SEQ ID NO:2 (RX 1040, p. 4, ll. 18-21; p. 9, ll. 5-8 and 13-17).

4       76. Further according to Ni's '842 specification, the full length DR5 lacks the  
5       methionine encoded by nucleotides 130-132 of SEQ ID NO: 1 (RX 1040,  
6       p. 11, ll. 28-32) and "may or may not include the leader sequence" (id., p.  
7       37, ll. 15-16).

8       Rauch argues that

9               a DNA sequence encoding a polypeptide "at least  
10              90% identical" to Rauch SEQ ID NO:2 would include  
11              (1) a DNA sequence encoding a polypeptide having  
12              the same sequence as residues 1 to 440 of Rauch  
13              SEQ ID NO:2; (2) a DNA sequence encoding a  
14              polypeptide having the same sequence as residues 1  
15              to 440 of Rauch SEQ ID NO:2 but for the substitution  
16              of 1 to 44 of the 440 residues; (3) a DNA sequence  
17              encoding a polypeptide having the same sequence as  
18              residues 1 to 440 of Rauch SEQ ID NO:2 but for the  
19              deletion of 1 to 44 residues; and (4) a DNA sequence  
20              encoding a polypeptide having the same sequence as  
21              residues 1 to 440 of Ni [sic] SEQ ID NO:2 but for the  
22              addition of 1 to 44 additional residues to the 440  
23              residues. [Paper 35, p. 5, ll. 1-10.]

24      In essence, Rauch's position is that "as long as a single species of a claim falls  
25      within the count, then that claim corresponds to the count" (id., p. 5, ll. 14-15).

26              "A claim corresponds to a count if the subject matter of the count, treated  
27      as prior art to the claim, would have anticipated or rendered obvious the subject  
28      matter of the claim." 37 CFR § 41.207(b)(2). A prior art species within a claimed  
29      genus reads on the generic claim and anticipates. In re Gostelli, 872 F.2d 1008,  
30      1010, 10 USPQ2d 1614, 1616 (Fed. Cir. 1989). However, a species claim is not  
31      necessarily obvious in light of a prior art disclosure of a genus. In re Baird, 16

1 F.3d 380, 382, 29 USPQ2d 1550, 1552 (Fed. Cir. 1994). In other words, the  
2 "earlier disclosure of a genus does not necessarily prevent the patenting of a  
3 species member of that genus." Eli Lilly & Co. v. Bd. of Regents of the Univ. of  
4 Washington, 334 F.3d 1264, 1270, 67 USPQ2d 1161, 1165 (Fed. Cir. 2003)  
5 (citations omitted).

6 Here, the subject matter of Count 1 is directed to a genus of functional  
7 proteins, i.e., purified TRAIL-R polypeptides having an amino acid sequence that  
8 is at least 90% identical to SEQ ID NO:2 of Rauch's involved '358 patent,  
9 wherein the polypeptides bind TRAIL (FF 11). Assuming without deciding that  
10 the isolated polypeptides of Ni claims 46, 55, 63, 64, 110 and 118 bind TRAIL,  
11 none of these claims recite an isolated polypeptide having an amino acid  
12 sequence identical to SEQ ID NO:2 of Rauch's '358 patent. Ni claims 46, 55, 63,  
13 64, 110 and 118 are directed to subgenera/species within the genus of Count 1.  
14 The genus of Count 1 does not anticipate the specific subgenera/species of Ni  
15 claims 46, 55, 63, 64, 110 and 118. For example, Ni claim 46 recites a subgenus  
16 (an isolated polypeptide comprising an amino acid sequence at least 95%  
17 identical to) within a subgenus (amino acids -50 to 360 of SEQ ID NO:2 of Ni's  
18 '842 application, wherein said polypeptide induces apoptosis) (FF 67). Simply  
19 showing that a subgenus/species claim falls within the subject matter of a generic  
20 count does not suffice to establish that the claim is anticipated or rendered  
21 obvious by the subject matter of the count. Rauch has not established why any  
22 of Ni claims 46, 55, 63, 64, 110 and 118 would be unpatentable over the subject  
23 matter of Count 1, i.e., why the subject matter of each of these claims is an

1 obvious subgenera/species within the generic subject matter of the count.

2 Therefore, Rauch has failed to meet its burden.

3 Based on the foregoing, Rauch substantive motion 2 is **denied**.

4 **VIII. Rauch Substantive Motion 1**

5 Pursuant to 37 CFR § 41.121(a)(1)(ii), Rauch moves to be accorded  
6 benefit for the purpose of priority of the (i) 13 February 1997 filing date of  
7 application 08/799,861 ("the '861 application," RX 1014), (ii) 12 March 1997 filing  
8 date of application 08/815,255 ("the '255 application," RX 1015), (iii) 28 March  
9 1997 filing date of application 08/829,536 ("the '536 application," RX 1016), and  
10 (iv) 4 June 1997 filing date of application 08/869,852 ("the '852 application," RX  
11 1017) (Paper 34). Ni opposes (Paper 47); Rauch replies (Paper 64).

12 The '392 application from which Rauch's involved '358 patent issued has  
13 already been accorded benefit of the 26 June 1997 filing date of Rauch's earlier  
14 filed '036 application (FF 7).

15 77. The '036 application is a continuation-in-part of the '852 application,  
16 which is a continuation-in-part of the '536 application, which is a  
17 continuation-in-part of the '255 application, which is a continuation-in-part  
18 of the '861 application (RX 1042, title page).

19 Benefit for the purpose of priority focuses on the subject matter of a count  
20 and only requires a constructive reduction to practice of a single embodiment  
21 within the scope of the count. Here, the subject matter of the count is directed to  
22 a purified TRAIL-R polypeptide having an amino acid sequence that is at least

1 90% identical to SEQ ID NO:2 of Rauch's involved '358 patent, wherein the  
2 polypeptide binds TRAIL (FF 11).

3 Rauch contends that the two earliest ('861 and '255) applications disclose a  
4 method of obtaining and purifying TRAIL-R protein, its ability to bind TRAIL, its  
5 molecular weight and partial amino acid sequences thereof sufficient to convince  
6 one of ordinary skill in the art that Rauch had possession of an isolated, purified  
7 TRAIL-R protein which inherently has an amino acid sequence at least 90%  
8 identical to SEQ ID NO:2 of the '358 patent (Paper 34, pp. 5-8). Rauch further  
9 contends that the later two ('536 and '852) applications additionally disclose the  
10 full-length amino acid sequence of TRAIL-R which is identical to the amino acid  
11 sequence set forth in SEQ ID NO:2 of the '358 patent (Paper 34, pp. 8-10).

12 Ni argues that none of the four applications disclose any utility for TRAIL-R  
13 protein and, therefore, fail the how-to-use prong of the enablement requirement  
14 of 35 U.S.C. § 112, first paragraph (Paper 47, p. 2). As to the two earliest ('861  
15 and '255) applications, Ni further argues that (a) the disclosed purification method  
16 results in a mixture of TRAIL-binding proteins, (b) the disclosed partial amino  
17 acid sequence contains amino acids not present in SEQ ID NO:2 of the '358  
18 patent, (c) the disclosed molecular weight is insufficient to differentiate TRAIL-R  
19 protein from other TRAIL-binding proteins, and (d) the amino acid sequence of  
20 the "purified" protein is less than 90% identical to SEQ ID NO:2 of the '358 patent  
21 (Paper 47, pp. 8-22).

22 78. It is undisputed that the TRAIL-R protein having the amino acid sequence  
23 set forth in SEQ ID NO:2 of the '358 patent is the 440 amino acid

1 isoform<sup>12</sup> of a TNF receptor protein alternatively referred to in the art as  
2 TR-2, DR5, Apo-2, TRICK2 and KILLER (see Paper 47, p. B-1 where Ni  
3 admits Rauch SMFs 1 and 6 as set forth in Paper 34, p. 12).

4 79. According to the '358 patent, the TRAIL-R protein of SEQ ID NO:2 is a  
5 full-length protein which includes an N-terminal signal peptide<sup>13</sup> (RX  
6 1042, c. 2, ll. 54-56).

7 80. Further according to the '358 patent, the signal peptide of the 440 amino  
8 acid full-length TRAIL-R protein is predicted to correspond to amino acids  
9 1 to 51 or 1 to 56 of SEQ ID NO:2 (RX 1041, c. 2, ll. 58-62; c. 3., ll. 1-12).

10 **A. The '852 (RX 1017) and '536 (RX 1016) applications**

11 81. According to the '852 specification, TRAIL or "TNF-related apoptosis-  
12 inducing ligand" is a member of the tumor necrosis factor (TNF) family of  
13 ligands and TRAIL-R binds TRAIL (RX 1017, p. 1, ll. 16-18 and 26-28; p.  
14 2, ll. 9-10).

15 82. According to the '536 specification, TRAIL or "TNF-related apoptosis-  
16 inducing ligand" is a member of the tumor necrosis factor (TNF) family of  
17 ligands and TRAIL-R binds TRAIL (RX 1016, p. 1, ll. 15-17 and 25-27; p.  
18 2, ll. 9-10).

19 83. Further according to the '852 specification, "[c]ertain uses of TRAIL-R  
20 flow from this ability to bind TRAIL, . . . TRAIL-R finds use in inhibiting

---

<sup>12</sup> An isoform is a variant of the same protein between various tissues, development stages, etc. with some small differences, usually a splice variant or the product of some posttranslational modification.

<sup>13</sup> A signal peptide (or leader sequence) is a continuous sequence of amino acids, normally at the N-terminus of a protein, that targets the full-length protein to its eventual location in a cell and is then cleaved off (see generally, MCB, p. 652) (copy enclosed).

- 1 biological activities of TRAIL, or in purifying TRAIL by affinity  
2 chromatography, for example" (RX 1017, p. 2, ll. 10-12; these and  
3 additional uses are set forth at p. 20, l. 15 - p. 25, l. 11).
- 4 84. Further according to the '536 specification, "[c]ertain uses of TRAIL-R  
5 flow from this ability to bind TRAIL, . . . TRAIL-R finds use in inhibiting  
6 biological activities of TRAIL, or in purifying TRAIL by affinity  
7 chromatography, for example" (RX 1016, p. 2, ll. 10-12; these and  
8 additional uses are set forth at p. 13, l. 34 - p. 18, l. 26).
- 9 85. Example 6 in the '852 specification is said to demonstrate the ability of  
10 full length human TRAIL-R to bind TRAIL (RX 1017, p. 35, l. 4 - p. 36, l.  
11 13).
- 12 86. The '536 specification explicitly states that TRAIL-R binds TRAIL (RX  
13 1016, p. 1, ll. 25-27; p. 13, l. 36; p. 22, l. 25 - p. 23, l. 22).
- 14 87. SEQ ID NO:1 of the '852 application is said to show a human foreskin  
15 fibroblast derived TRAIL-R cDNA encoding a protein having the amino  
16 acid sequence set forth in SEQ ID NO:2 of the '852 application (RX 1017,  
17 p. 33, ll. 17-21; pp. 39-43).
- 18 88. Figure 2 of the '536 application is said to show a human foreskin  
19 fibroblast derived TRAIL-R cDNA encoding a protein having the amino  
20 acid sequence set forth in Figure 3 of the '536 application (RX 1016, p.  
21 24, ll. 29-33).
- 22 89. It is undisputed that the full length TRAIL-R amino acid sequence set  
23 forth in SEQ ID NO:2 of the '852 application is identical to the full length

1 TRAIL-R amino acid sequence set forth in SEQ ID NO:2 of the '358  
2 patent (compare RX 1017, pp. 42-43, and RX 1042, cc. 33-35; see Paper  
3 47, p. B-3 where Ni admits Rauch SMF 27 as set forth in Paper 34, p.  
4 17).

5 90. It is undisputed that the full length TRAIL-R amino acid sequence set  
6 forth in Figure 3 of the '536 application is identical to the full length  
7 TRAIL-R amino acid sequence set forth in SEQ ID NO:2 of the '358  
8 patent (compare RX 1016, Figure 3, and RX 1042, cc. 33-35; see Paper  
9 47, p. B-3 where Ni admits Rauch SMF 24 as set forth in Paper 34, p.  
10 17).

11 91. Thus, the '852 and '536 applications each describe an embodiment within  
12 the scope of Count 1, i.e., a a purified TRAIL-R polypeptide having an  
13 amino acid sequence that is at least 90% identical to SEQ ID NO:2 of  
14 Rauch's involved '358 patent (FFs 87-90), wherein the polypeptide binds .  
15 TRAIL (FFs 81-86).

16 Relying on Rasmusson v. SmithKline Beecham Corp., 413 F.3d 1318, 75  
17 USPQ2d 1297 (Fed. Cir. 2005), Ni argues that neither the '852 nor the '536  
18 application discloses any utility for TRAIL-R protein and, therefore, fail the how-  
19 to-use prong of the enablement requirement of 35 U.S.C. § 112, first paragraph  
20 (Paper 47, p. 2 and p. 7, ¶ 2). Specifically, Ni argues that "[n]owhere in Rauch  
21 Substantive Motion 1 does Party Rauch even imply that its earlier applications  
22 discloses [sic] a utility for a polypeptide of the count" (Paper 47, p. 7, ¶ 4).

1 In essence, the only opposition raised by Ni is whether the '852 and '536  
2 applications disclose an adequate utility/enablement for a polypeptide within the  
3 scope of the count. First, Count 1 explicitly describes a utility for a polypeptide  
4 within its scope, i.e., the polypeptide binds TRAIL. Second, Rauch asserted this  
5 utility/enablement (Paper 34, p. 8, ¶ 3 - p. 10, ¶ 1) and pointed to express  
6 descriptive support of an embodiment within the scope of Count 1 in the '852 and  
7 '536 applications in Appendices F and E, respectively, of its motion. Third, the  
8 '852 and '536 specifications explicitly state that TRAIL-R binds TRAIL (FFs 81-  
9 86). Fourth, our finding that the '852 and '536 applications describe and enable  
10 an embodiment within the scope of Count 1 is not inconsistent with the holding in  
11 Rasmusson.

12 In Rasmusson both parties had interfering claims directed to methods of  
13 treating prostate cancer comprising administering finasteride, a selective 5- $\alpha$ -  
14 reductase inhibitor. An interference was declared by the Board of Patent  
15 Appeals and Interferences (the Board). Rasmusson was involved in the  
16 interference on the basis of an application which claimed priority to eight earlier  
17 filed applications. SmithKline Beecham Corp. was involved in the interference on  
18 the basis of two patents and corresponding reissue applications. On appeal from  
19 the decision of the Board, the Federal Circuit affirmed the Board's holding that  
20 Rasmusson was not entitled to benefit for the purpose of priority of the filing  
21 dates of the eight earlier filed applications. Citing In re Brana, 51 F.3d 1560, 34  
22 USPQ2d 1436 (Fed. Cir. 1995), the court said "a specification disclosure which  
23 contains a teaching of the manner and process of making and using the invention

1 . . . must be taken as in compliance with the enabling requirement of the first  
2 paragraph of § 112 unless there is a reason to doubt the objective truth of the  
3 statements contained therein which must be relied on for enabling support"  
4 (Rasmusson, 413 F.3d at 1323, 75 USPQ2d at 1300, emphasis added). The  
5 court affirmed the Board's finding that one of ordinary skill in the art would not  
6 have believed that finasteride was effective in treating prostate cancer in light of  
7 the state of the art at the relevant time and because Rasmusson had failed to  
8 provide experimental proof demonstrating the effectiveness of the invention (id.,  
9 413 F.3d at 1324-25, 75 USPQ2d at 1301).

10 Here, the '852 and '536 specifications explicitly state that TRAIL-R binds  
11 TRAIL (FFs 81-82). The '852 and '536 specifications further describe certain  
12 uses of TRAIL-R based on its ability to bind TRAIL, e.g., using TRAIL-R to purify  
13 TRAIL by affinity chromatography (FFs 83-84). Ni has not pointed to evidence of  
14 record which raises doubts as to the objective truth of these statements in either  
15 the '852 or '536 specifications, as was the case in Rasmusson. For example, Ni  
16 does not argue or provide evidence that a receptor protein that binds a ligand  
17 could not be used to purify the ligand by affinity chromatography at the time the  
18 '852 or '536 application was filed. Alternatively, Ni does not provide any  
19 evidence that the TRAIL-R protein set forth in SEQ ID NO:2 and Figure 3 of the  
20 '852 and '536 applications, respectively, does not bind TRAIL. Moreover, Ni  
21 does not argue that the '852 and '536 applications fail to disclose any utility for  
22 the TRAIL-R polypeptide set forth their respective SEQ ID NO:2 and Figure 3  
23 (FFs 87-88). In short, Rauch has described how to use a purified TRAIL-R

1 polypeptide within the scope of the count, i.e., TRAIL-R binds TRAIL (Paper 34,  
2 p. 8, ¶ 3 - p. 10, ¶ 1), and Ni has not provided any basis to doubt the objective  
3 truth of express statements in the '852 and '536 specifications that the TRAIL-R  
4 of their respective SEQ ID NO:2 and Figure 3 is useful to bind TRAIL.

5 Based on the foregoing, Rauch substantive motion 1 is **granted** as to the  
6 '852 and '536 applications.

7 **B. The '255 (RX 1015) and '861 (RX 1014) applications**

8 92. According to the '255 specification, TRAIL-R is a protein which binds  
9 TRAIL and, thus, finds uses in affinity chromatography purification of  
10 TRAIL and in inhibiting biological activities of TRAIL (RX 1015, p. 1, ¶ 5).

11 93. The '255 specification states that Example 1 discloses the isolation and  
12 purification of human TRAIL-R protein with a molecular weight of about  
13 52 kD from the cell membranes of Jurkat cells (RX 1015, p. 16, ¶ 3).

14 94. Specifically, "Jurkat cells are disrupted, and the subsequent purification  
15 process includes affinity chromatography (employing a chromatography  
16 matrix containing TRAIL), and reversed phase HPLC" (RX 1015, p. 4, ¶  
17 5).

18 95. Further according to the '255 specification, Example 2 discloses the  
19 amino acid sequences of tryptic fragments of TRAIL-R protein purified  
20 from Jurkat cells and from PS-1 cells (RX 1015, p. 18, ¶ 4 - p. 19, ¶ 1).

21 96. TRAIL-R protein purified from Jurkat cells and from PS-1 cells were both  
22 said to yield a tryptic fragment having the same amino acid sequence,  
23 i.e., VPANEGD (RX 1015, p. 19, ¶ 1).

- 1        97. Two other tryptic fragments obtained from TRAIL-R protein purified from  
2        PS-1 cells were said to have amino acid sequences of VCEC and  
3        SGEVELSSV, respectively (RX 1015, p. 19, ¶ 2).
- 4        98. Example 3 of the '255 specification is said to describe isolating and  
5        amplifying a TRAIL-R DNA fragment from a PS-1 cell cDNA (RX 1015.,  
6        p. 19, ¶ 3).
- 7        99. Figure 1 of the '255 application is said to show the nucleotide and  
8        encoded amino acids sequences of the isolated TRAIL-R DNA fragment:  
9        ETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLX  
10       TML (RX 1015, p. 19, p. 19, ¶ 3; p. 24).
- 11       100.      According to the '861 specification, TRAIL-R is a protein which  
12       binds TRAIL and, thus, finds uses in affinity chromatography purification  
13       of TRAIL and in inhibiting biological activities of TRAIL (RX 1014, ll. 26-  
14       30)
- 15       101.      The '861 specification states that Example 1 discloses the isolation  
16       and purification of human TRAIL-R protein with a molecular weight of  
17       about 52 kD from the cell membranes of Jurkat cells (RX 1014, p. 15, ll.  
18       27-34).
- 19       102.      Specifically, "Jurkat cells are disrupted, and the subsequent  
20       purification process includes affinity chromatography (employing a  
21       chromatography matrix containing TRAIL), and reversed phase HPLC"  
22       (RX 1014, p. 4, ll. 5-7).

1           103.       Further according to the '861 specification, Example 2 discloses the  
2                   amino acid sequences of tryptic fragments of TRAIL-R protein purified  
3                   from Jurkat cells and from PS-1 cells (RX 1014, p. 18, ll. 7-31).

4           104.       TRAIL-R protein purified from Jurkat cells and from PS-1 cells were  
5                   both said to yield a tryptic fragment having the same amino acid  
6                   sequence, i.e., VPANEGD (RX 1014, p. 18, ll. 7-25).

7           105.       Two other tryptic fragments obtained from TRAIL-R protein purified  
8                   from PS-1 cells were said to have amino acid sequences of VCEC and  
9                   SGEVELSSV, respectively (RX 1014, p. 18, ll. 27-32).

10          Rauch acknowledges that, unlike the '852 and the '536 applications, neither  
11          the '255 nor the '861 applications disclose the full amino acid sequence of  
12          TRAIL-R as presented in SEQ ID NO:2 of the '358 patent (Paper 34, p. 5, ¶ 3  
13          and p. 7, ¶ 1). Rauch argues that (a) the isolated, purified TRAIL-R protein  
14          disclosed in the '255 and '861 applications inherently has an amino acid  
15          sequence at least 90% identical to that set forth in SEQ ID NO:2 of the '358  
16          patent and (b) the '255 and '861 applications disclose that TRAIL-R binds TRAIL  
17          (Paper 34, p. 8, ¶ 1 and ¶ bridging pp. 7-8). Rauch relies on the testimony of Dr.  
18          Cheng in support of its position.

19          106.       According to Dr. Cheng, the disclosure of the '861 application,  
20                   specifically Examples 1 and 2, "would lead one of ordinary skill in the art  
21                   to conclude that the inventors had possession of an isolated, purified  
22                   protein that bound TRAIL at the time the '861 Application was filed" from  
23                   the membranes of Jurkat cells, said protein having a molecular weight of

1           about 50-55 kD as determined by SDS-PAGE and a partial amino acid  
2           sequence of VPANEGD (RX 1039, ¶ 8).

3       107.       Further according to Dr. Cheng, the disclosure of the '255  
4           application is substantially the same as that of the '861 application and  
5           additionally discloses a 51 amino acid sequence bearing significant  
6           homology to the death domains found in TNF receptor proteins TNFR1  
7           and Fas (RX 1039, ¶ 10).

8       108.       Still further according to Dr. Cheng,  
9                   identification of a putative death domain in TRAIL-R,  
10                  combined with the experimental data previously  
11                  disclosed in the '861 Application showing the isolation  
12                  and purification of TRAIL-R, its molecular weight, and  
13                  its ability to bind TRAIL, would be sufficient to convey  
14                  to one of ordinary skill in the art that the inventors  
15                  were in possession of a TRAIL receptor belonging to  
16                  the TNFR family at the time the '255 Application was  
17                  filed in March of 1997 (RX 1039, ¶ 10).

18       109.       Dr. Cheng concluded that a skilled artisan would recognize that the  
19           isolated, purified TRAIL-R protein disclosed in the '861 and '255  
20           applications had an amino acid sequence which was later determined to  
21           be a TR-2 sequence which is at least 90% identical to the amino acid  
22           sequence set forth in Rauch SEQ ID NO:2 as required by Count 1 (RX  
23           1039, ¶¶ 8-9).

24       Ni contends that Rauch's inherency theory is flawed. Specifically, Ni argues  
25       that any TRAIL-R protein purified by the method disclosed in the respective  
26       Example 1 of the '861 and '255 specifications is necessarily the mature form of a  
27       TRAIL-R protein, which lacks its leader sequence (signal peptide) and, therefore,

1 would not have an amino acid sequence that is at least 90% identical to the  
2 amino acid sequence of SEQ ID NO:2 of the '358 patent. [Paper 47, p. 4, ¶ 2.]

3 110. TRAIL-R protein is expressed on the membranes of Jurkat cells  
4 (see e.g., RX 2137, p. 700, c. 2, ¶ 2).

5 111. The isolation and purification method disclosed in Example 1 of the  
6 '861 and '255 applications and of the '358 patent are essentially identical  
7 (compare Example 1 in each of RX 1015 (pp. 16-18), RX 1014 (pp. 15-  
8 17) and RX 1042 (cc. 23-25)).

9 112. Dr. Cheng also testified that Example 1 of the '861 application and  
10 the '358 patent are essentially identical, but for minor spelling  
11 differences, e.g., abbreviating California as "CA" in one and "Calif" in the  
12 other (NX 2124, p. 98, l. 3 - p. 99, l. 17).

13 113. According to Dr. Cheng, the method of Example 1 would yield  
14 mostly mature TRAIL-R protein because it was obtained from Jurkat cell  
15 membranes (NX 2124, p. 93, l. 13 - p. 95, l. 8; p. 101, ll. 3-7; p. 103, ll. 8-  
16 12; p. 104, l. 17- p. 105, l. 3).

17 114. According to the involved '358 patent, analysis of tryptic fragments  
18 obtained from a mature TRAIL-R protein shows that its N-terminal is  
19 amino acid residue 56 of SEQ ID NO:2, i.e., that a 55 amino acid  
20 signal peptide was cleaved off of full length TRAIL-R protein when  
21 TRAIL-R was inserted into the cell membrane (RX 1042, c. 3, ll. 1-32).

22 115. Dr. Cheng testified that a mature form of TRAIL-R protein having  
23 385 amino acid residues (i.e., missing its 55 amino acid leader

1           sequence) is 87.5 percent identical to 440 amino acid full length  
2           TRAIL-R protein (NX 2124, p. 95, I. 25 - p. 97, I. 23 and p. 115, II. 10-  
3           21 (dividing 385 by 440 and multiplying by 100 to yield %)).

4           116.   However, according to Dr. Cheng, simply dividing the number of  
5           identical residues in two proteins by the number of residues in the  
6           longer protein was neither the only way of determining percent identity  
7           between the proteins nor the preferred method (NX 2124, p. 108, II. 20-  
8           24).

9           117.   While the '358 patent specification does not define "percent  
10          identity" as that term is used in its claims, the '358 specification states  
11          that "percent identity may be determined, for example, by comparing  
12          sequence information using the GAP computer program, version 6.0  
13          described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) (RX  
14          1042. c. 6, I. 65 - c. 7, I. 1).

15          118.   In Dr. Cheng's opinion, the mature and full length forms of TRAIL-R  
16          are the same protein because they are from the same gene (NX 2124,  
17          p. 101, II. 12-24).

18          119.   Neither Dr. Cheng nor Ni determined what percent identity a mature  
19          form of TRAIL-R protein having 385 amino acid residues would have to  
20          440 amino acid full length TRAIL-R protein set forth in SEQ ID NO:2 of  
21          the '358 patent using the GAP computer program, version 6.0  
22          described by Devereux et al. (*Nucl. Acids Res.* 12:387, 1984) set forth  
23          in the '358 patent (RX 1042. c. 6, I. 65 - c. 7, I. 1).

1           The count requires, in relevant part, an isolated TRAIL-R polypeptide  
2   having an amino acid sequence that is at least 90% identical to SEQ ID NO:2 of  
3   the '358 patent. Rauch contends that the isolated, purified TRAIL-R protein  
4   disclosed in the '255 and '861 applications inherently satisfies this limitation. As  
5   stated in In re Oelrich, 666 F.2d 578, 581, 212 USPQ 323, 326 (CCPA 1981)  
6   (quoting Hansgird v. Kemmer, 102 F.2d 212, 214, 40 USPQ 665, 667 (CCPA  
7   1994)), "[i]nherence, however, may not be established by probability or  
8   possibilities. The mere fact that a certain thing may result from a given set of  
9   circumstances is not sufficient."

10           It is clear from Dr. Cheng's testimony that there are a number of ways of  
11   calculating percent identity between two given amino acid sequences, each of  
12   which may yield a different result. By at least one calculation, a TRAIL-R protein  
13   obtained from Jurkat cell membranes (as described in Rauch's '255 and '861  
14   applications) would be less than 90% identical to SEQ ID NO:2 of the '358 patent  
15   as required by Count 1 (i.e., Dr. Cheng calculated an 87.5 % identity (FF 115)).  
16   Using a different method may give a different result (e.g., Tartaglia calculated  
17   29% identity over 45 amino acids, but extended the region of homology an  
18   additional 20 amino acids by introducing a single amino acid gap in one of the  
19   sequences (FF 46)). While Dr. Cheng has stated that some methods of  
20   calculating percent identity are preferred over others, neither Dr. Cheng nor  
21   Rauch has pointed to evidence of record establishing an art recognized standard  
22   method of calculating percent identity between amino acid sequences.  
23   Furthermore, neither Dr. Cheng nor Rauch has pointed to an art recognized

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 56  
Paper 101

1 method of calculation which establishes at least a 90% identity between the  
2 amino acid sequences. Additionally, software programs used to calculate  
3 percent identity are programmed to create different alignments based on different  
4 methods (FF 43). In short, not only do different methods of calculating percent  
5 identity give different results, but also apparently there is no standard method in  
6 the art for calculating percent identity. Thus, one method might yield a percent  
7 identity that falls within the count, while another method might not. Since the  
8 specification of the '358 patent does not define how to determine "percent  
9 identity" (FF 117), there is no defined method for determining whether a  
10 particular amino acid sequence is "at least 90% identical" to SEQ ID NO:2 of the  
11 '358 patent as required by the count. Moreover, to the extent the '358 patent  
12 suggests that the GAP computer program, version 6.0 described by Devereux et  
13 al. (*Nucl. Acids Res.* 12:387, 1984) might be the preferred method for  
14 determining percent identity between two sequences (FF 117), neither Ni, Rauch  
15 nor Dr. Cheng have shown that applying this calculation will result in at least 90%  
16 sequence identity between mature and full length TRAIL-R proteins. Therefore,  
17 Rauch has failed to establish that the isolated, purified TRAIL-R protein disclosed  
18 in the '255 and '861 applications inherently has an amino acid sequence at least  
19 90% identical to that set forth in SEQ ID NO:2 of the '358 patent. Consequently,  
20 Rauch substantive motion 1 is **denied** as to the '255 and '861 applications.

21 Ni's argument that the '255 and '863 applications fail to satisfy the how-to-  
22 use requirement of § 112, first paragraph, because the '255 and '863 applications  
23 allegedly fail to disclose any utility for the described TRAIL-R protein is not

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 57  
Paper 101

1 persuasive in view of their respective disclosures (FFs 92 and 100) and  
2 Appendices D and C, respectively, attached to Paper 34 for substantially the  
3 same reasons set forth above in regard to the '536 and '852 applications. It is  
4 unnecessary to reach the merits of Ni's two remaining arguments based on  
5 molecular weight and alleged errors in amino acid sequences. In particular, we  
6 need not consider what effect errors in amino acid sequencing might have on the  
7 percent identity between the sequence containing some errors and SEQ ID NO:2  
8 of the '358 patent.

9 Based on the foregoing, Rauch substantive motion 1 is **granted** to the  
10 extent that Rauch is accorded benefit for purposes of priority of the 4 June 1997  
11 and 28 March 1997 filing dates of applications 08/869,852 and 08/829,536,  
12 respectively, and **otherwise denied**.

13 **IX. Ni Substantive Motion 3**

14 Pursuant to 37 CFR § 41.121(a)(1)(iii) and the Order issued 29 November  
15 2005 (Paper 26), Ni seeks judgment that all of Rauch's involved claims, claims 1,  
16 4-6, 8-11, 17-19, 26-28, 34, 37, 38 and 40, are unpatentable under 35 U.S.C.  
17 § 102(e) as anticipated by U.S. Patent 6,872,568 ("Ni's '568 patent," NX 2004)  
18 (Paper 31). Rauch opposes (Paper 54); Ni replies (Paper 62).

19 120. Ni's '568 patent issued from application 09/565,009 ("the '009  
20 application"), filed 4 May 2000 (NX 2004, title page (21), (22), (75)).

21 121. The '009 application is said to be a continuation-in-part of  
22 application 09/042,583 ("the '583 application," NX 2024), filed 17 March  
23 1998 (NX 2004, title page (63)).

1           122.       When the '583 application was filed, Ni claimed benefit under 35  
2           U.S.C. § 119(e) to provisional applications 60/040,846 (NX 2042) and  
3           60/054,021 (NX 2056), filed 17 March 1997 and 29 July 1997,  
4           respectively (NX 2024, p. 1, ll. 12-14).

5           123.       Rauch's involved '358 patent issued from the '392 application, filed  
6           25 May 2000 (FF 6), after the filing of the '009 application.

7           124.       According to the '392 application, the '392 application is

8           (i)       a divisional of the '036 application (RX 1018), filed 26 June 1997,

9           (ii)       a continuation-in-part of the '852 application (RX 1017), filed 4 June  
10          1997,

11          (iii)       a continuation-in-part of the '536 application (RX 1016), filed 28  
12          March 1997,

13          (iv)       a continuation-in-part of the '255 application (RX 1015), filed 12  
14          March 1997,

15          (v)       a continuation-in-part of the '861 application (RX 1014), filed 13  
16          February 1997 (RX 1012, title sheet (60)).

17          Ni contends that Rauch's involved '358 patent claims are unpatentable under  
18          35 U.S.C. § 102(e) based on Ni's '568 patent (Paper 31, p. 2, ¶ 4). Ni's '568  
19          patent issued from an application filed three weeks before Rauch's application  
20          which issued as the '358 patent was filed (FFs 120 and 123). Therefore, on its  
21          face, the '568 patent is prior art to Rauch's involved claims. However, both Ni  
22          and Rauch assert that their respective '568 patent reference and involved claims  
23          are entitled to benefit of the filing dates of a number of earlier applications (FFs

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 59  
Paper 101

1 121, 122 and 124). Specifically, Ni argues that Rauch's claims are not entitled to  
2 a priority date any earlier than the 28 March 1997 filing date of Rauch's '536  
3 application, while Ni's '568 patent is entitled to the 17 March 1997 filing date of its  
4 '846 application (Paper 31, p. 8, ¶ 1 and p. 11, ¶ 3). Therefore, before deciding  
5 whether the disclosure of Ni's '568 patent anticipates the subject matter of  
6 Rauch's claims, we must first decide, as a matter of law, whether Ni's '568 patent  
7 and Rauch's '358 patent are entitled to the filing date of one or more of the  
8 applications to which they have claimed priority.

9 For prior art purposes, a patent is entitled to benefit of the filing date of a  
10 parent application as to all subject matter carried over into the patent from the  
11 parent application when the parent application discloses the invention claimed in  
12 the reference patent pursuant to 35 U.S.C. § 120 (and related statutes). In re  
13 Wertheim, 646 F.2d 527, 539, 209 USPQ 554, 565-66 (CCPA 1981). According  
14 to § 120, a subsequent application is permitted to relate back to the filing date of  
15 a prior application disclosing the same invention if the subsequent application is  
16 for an invention disclosed in the manner provided by the first paragraph of 35  
17 U.S.C. § 112, is submitted by the same inventor, is filed before the abandonment  
18 of the first application and specifically refers to the parent application. To satisfy  
19 the requirements of § 112, there must be a written description and an enabling  
20 disclosure of the full scope of the claimed subject matter. Warner-Lambert Co.,  
21 v. Teva Pharmaceuticals USA, Inc., 418 F.3d 1326, 1336-37, 75 USPQ2d 1865,  
22 1871-72 (Fed. Cir. 2005) (full scope of claims must be enabled); Pandrol USA,  
23 LP v. Airboss Railway Products, Inc., 424 F.3d 1161, 1165, 76 USPQ2d 1524,

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 60  
Paper 101

1 1526 (Fed. Cir. 2005) (written description must show possession of the claimed  
2 invention). Moreover, to get the benefit of the filing date of an earlier application  
3 under § 120 (and related statutes) where there is a chain of applications, there  
4 must be a chain of copending applications each of which satisfies the  
5 requirements of § 112, first paragraph, for the claimed subject matter. In re  
6 Hogan, 559 F.2d 595, 609, 194 USPQ 527, 540 (CCPA 1977). Thus, to the  
7 extent that a continuation-in-part application adds new matter, claims that are  
8 dependent upon the new matter are only entitled to the filing date of the  
9 continuation-in-part application and not that of the parent application.

10 Ni's '568 patent issued from a continuation-in-part application (the '009  
11 application) of parent application 09/042,583 (FFs 120 and 121) which claimed  
12 § 119(e) benefit of two provisional applications, 60/054,021 and 60/040,846 (FF  
13 122). Thus, in order for Ni's '568 patent to qualify as prior art § 102(e)(2) as of  
14 the 17 March 1997 filing date of its '846 application, Ni must show (1) that the  
15 subject matter claimed in the '568 patent was disclosed in the '583 parent  
16 application and in the '846 provisional application and (2) that the subject matter  
17 relied upon in the '846 provisional application was carried forward into the '583  
18 parent application and into the '568 patent.

19 Ni fails to make either showing.

20 125. The '568 patent claims isolated antibodies or fragments thereof that  
21 specifically bind to a protein "consisting of amino acid residues 1 to 133  
22 of SEQ ID NO:2" or to "the extracellular domain of the protein encoded  
23 by the cDNA contained in ATCC Deposit No. 97920," isolated cells and

1           hybridomas producing said antibodies/fragments, and methods of  
2           detecting DR5 using said antibodies/fragments (NX 2004, cc. 157-162).

3           Ni has neither argued nor pointed out where the antibody-based subject  
4           matter claimed in the '568 patent is disclosed in the '583 parent application or in  
5           either the '021 or '846 provisional application. The '568 patent was based on a  
6           continuation-in-part application and, therefore, presumptively contains additional  
7           and/or different subject matter than the '583 parent application. Ni has neither  
8           argued nor pointed out where the subject matter of either provisional application  
9           relied upon was carried forward into the '583 parent application and into the '568  
10          patent.

11          Ni simply asserts that the '568 patent issued from the '009 application which  
12          claimed priority as a continuation-in-part of the '583 application which claimed  
13          priority to the '021 and '846 provisional applications (Paper 31, ¶ 2). According to  
14          Ni, the '846 application "contains the entire nucleic acid sequence and the  
15          polypeptide sequence encoded thereby of a human DR5 protein" (Paper 31, p. 9,  
16          ¶ 1 (citations to SMF omitted)). The main focus of Ni's arguments is on  
17          disclosure in the '846 provisional application alleged to disclose the subject  
18          matter of Rauch's involved claims. There is little, if any, discussion of the claims  
19          of the '583 parent application and no argument or assertion that either the '583 or  
20          '846 application provides § 112, first paragraph, support for the claimed subject  
21          matter of the '568 patent. Thus, Ni has failed as matter of law to establish prima  
22          facie that its '568 patent is entitled to the filing date of the '583 parent application  
23          or either the '021 or '846 provisional application. Consequently, based on this

1 record, the '568 patent has only been shown to be entitled to a filing date of 4  
2 May 2000 for prior art purposes.

3       Additionally, we do not see how the filing date of either the '021 or '846  
4 provisional applications can be accorded to the '568 patent as its § 102(e) filing  
5 date. First, provisional applications were established to place domestic  
6 applicants on equal footing with foreign applicants with respect to rights of  
7 priority. 35 U.S.C. § 119(e). Section 102(e) of title 35 provides, in relevant part,  
8 that "A person shall be entitled to a patent unless ... (e) the invention was  
9 described in ... (2) a patent granted on an application for patent by another filed  
10 in the United States before the invention by the applicant for patent ...". Here, the  
11 reference being relied upon to show unpatentability under § 102(e) is the '568  
12 patent, not the '021 or '846 provisional application. Second, in reaching its  
13 conclusion in Wertheim<sup>14</sup> that a subsequent application is permitted to relate  
14 back to the filing date of a prior application disclosing the same invention if the  
15 subsequent application is for an invention disclosed in the manner provided by  
16 the first paragraph of 35 U.S.C. § 112, the CCPA stated:

---

<sup>14</sup> In Wertheim, the examiner made a 35 U.S.C. § 103 rejection over a U.S. patent to Pfluger. The Pfluger patent (Pfluger IV) was the child of a string of abandoned parent applications (Pfluger I, the first application, Pfluger II and III, both continuations-in-part). Pfluger IV was a continuation of Pfluger III. The court characterized the contents of the applications as follows: Pfluger I - subject matter A; Pfluger II - subject matter AB; Pfluger III, subject matter ABC; and, Pfluger IV - subject matter ABC. ABC anticipated the claims of the application being examined, but the filing date of Pfluger III was later than the application filing date. The Examiner reached back to subject matter A in Pfluger I and combined this disclosure with another reference to establish obviousness under § 103. The court held that the Examiner impermissibly carried over subject matter A and should have instead determined which of the parent applications contained the subject matter which made Pfluger patentable. Only if subject matter B and C were not claimed, or at least not critical to the patentability of Pfluger IV could Pfluger IV rely on the filing date of Pfluger I. The court determined that Pfluger IV was only entitled to the filing date of Pfluger III and reversed the rejection, noting that the added new matter C was critical to the claims of the issued patent.

1           The dictum in Lund, *supra*, that

2                         \* \* \* the continuation-in-part application is  
3                         entitled to the filing date of the parent  
4                         application as to all subject matter *carried over*  
5                         into it from the parent application \* \* \* for  
6                         purposes of \* \* \* utilizing the *patent* disclosure  
7                         as evidence to defeat another's right to a  
8                         patent \* \* \* [emphasis in the original]

9           is hereby modified to further include the requirement  
10           that the application, the filing date of which is needed  
11           to make a rejection must disclose, pursuant to  
12           §§ 120/112, the invention claimed in the reference  
13           patent. Where continuation-in-part applications are  
14           involved, the logic of the Milburn holding as to secret  
15           prior art would otherwise be inapplicable. Without the  
16           presence of a patentable invention, no patent could  
17           issue "but for the delays of" the PTO.

18   Wertheim, 646 F.2d at 539, 209 USPQ at 565-66. Here, Ni has not shown that  
19   the subject matter claimed in the '568 patent could have issued earlier "but for  
20   the delays" of the PTO and, therefore, the '568 patent was entitled, as a matter of  
21   law, to the filing of either provisional application as its § 102(e) filing date. No  
22   U.S. patent can issue from a provisional application filed under § 111(b).  
23   Therefore, any time a provisional application is pending is not a delay that can be  
24   attributed to the PTO under the Milburn delay theory. Again, Ni has failed as  
25   matter of law to establish prima facie that its '568 patent is entitled to the filing  
26   date of either the '021 or '846 provisional application.

27           Rauch, on the other hand, appears to have confused benefit accorded for  
28   purpose of priority in an interference contest with benefit accorded under § 120  
29   (see e.g., Paper 54, p. 17). Nonetheless, Rauch has provided detailed claim  
30   charts said to show where the claimed subject matter of Rauch's involved '358  
31   patent is supported by each of its asserted priority applications (Paper 54,

1 Appendices D through H). For example, Rauch asserts that Appendix H (Paper  
2 54, pp. 143-166) describes where the '036 parent application, said to be a  
3 divisional of the application from which Rauch's involved '358 patent issued (FFs  
4 122 and 123), provides support for each claim of Rauch's involved '358 patent on  
5 a claim-by-claim basis. Based on the evidence submitted, Rauch has prima facie  
6 established that its involved claims are at least entitled to benefit of the 26 June  
7 1997 filing date of its '036 parent application. Ni does not dispute Rauch's claim  
8 to benefit of the filing date of the '036 application (Paper 31, p. 8, ¶ 1 and p. 11, ¶  
9 3).

10 In summary, since the '568 patent has only been shown to be entitled to a  
11 filing date of 4 May 2000 for prior art purposes and Rauch's involved claims have  
12 been shown to be entitled to a filing date of at least 26 June 1997, the '568 patent  
13 does not qualify as prior art vis-à-vis Rauch's involved claims under § 102(e). It  
14 is not necessary to consider whether Rauch's involved claims are entitled to one  
15 or more of the filing dates of Rauch's still earlier filed '852, '536, '255 or '861  
16 application. Moreover, since the '568 patent has not been shown to be prior art  
17 under § 102(e), it is not necessary for us to consider the content of the '568  
18 patent.

19 Based on the foregoing, Ni substantive motion 3 is **denied**.

20 **X. Rauch Miscellaneous Motion 5**

21 Pursuant to 37 CFR § 41.155(c), Rauch seeks to exclude selected  
22 portions of the direct testimony of Dr. Reed that reference a person of ordinary  
23 skill in the art from evidence (NX 2103, ¶¶ 16, 19, 21-28, 30-43, 45-48, 50-52, 56

1 and 63-64), contending that his definition of ordinary skill "is so broad that it fails  
2 to limit 'one of ordinary skill in the art' to any substantive or realistic meaning of  
3 such person" (Paper 76, p. 5, ¶ 2). Thus, Rauch argues, any statement by Dr.  
4 Reed regarding what one of ordinary skill in the art would have known or  
5 understood in 1997 is irrelevant, lacking foundation, prejudicial and confusing  
6 (Paper 76, p. 6, ¶ 1). Rauch further seeks to exclude selected portions of the  
7 redirect testimony of Dr. Reed from evidence as improper redirect, leading and  
8 prejudicial (NX 2123, p. 169, ll. 2-21 and p. 172, l. 16 - p. 173, l. 13) (Paper 76, p.  
9 9, ¶ 2; pp. 11-12). Finally, Rauch seeks to exclude selected portions of the direct  
10 testimony of Dr. Andrew Badley (NX 2157, ¶¶ 26-27, 31-32 and 34-38), also  
11 contending that Dr. Badley's definition of a "person of ordinary skill in the art" is  
12 so flawed that any statement by Dr. Badley regarding what one of ordinary skill in  
13 the art would have known or understood in 1997 is irrelevant, lacking foundation,  
14 prejudicial and confusing (Paper 76, p. 13, ¶ 2 and p. 15, ¶ 1). Rauch further  
15 contends that Dr. Badley lacks sufficient expertise on the subject matter of his  
16 testimony (Paper 76, p. 16, ¶ 2).

17 126. Rauch timely filed its objections to the evidence sought to be  
18 excluded (RXs 1094 and 1095; NX 2123, p. 161; p. 166, l. 2; p. 169, ll. 10  
19 and 16; p. 172, l. 20; p. 173, ll. 7-8).

20 Rauch identifies the objected to testimony of Dr. Reed as submitted in  
21 support of Ni substantive motion 2, Ni reply 2, Ni reply 3 and Ni opposition 3 to  
22 Rauch substantive motion 3 (Paper 76, Appendix D). First, Rauch's arguments  
23 go to the weight to be accorded Dr. Reed's testimony based on the

1 reasonableness of his conclusions as assessed by one of ordinary skill in the art  
2 in view of the state of the art at the relevant time, not to its admissibility. Second,  
3 having considered the testimony of both Dr. Reed and Dr. Cheng, we credited  
4 the testimony of the latter over that of the former as discussed in our denial of the  
5 relevant portion of Ni substantive motions 2 and 3 and in our grant of the relevant  
6 portion of Rauch substantive motion 3. Therefore, Rauch substantive motion 5 is  
7 dismissed as moot to the extent it seeks to exclude selected portions of the direct  
8 and redirect testimony of Dr. Reed since we have not relied upon either the direct  
9 or redirect testimony of Dr. Reed to Rauch's detriment.

10 Rauch identifies the objected to testimony of Dr. Badley as submitted in  
11 support of Ni opposition 1 to Rauch substantive motion 1, Ni opposition 3 to  
12 Rauch substantive motion 3, Ni opposition 4 to Rauch substantive motion 4 and  
13 Ni reply 3. Again, Rauch's arguments go to the weight to be accorded Dr.  
14 Badley's testimony based on the reasonableness of his conclusions as assessed  
15 by one of ordinary skill in the art in view of the state of the art at the relevant time,  
16 not to its admissibility. Since Rauch substantive motion 4 was dismissed as  
17 moot, we did not reach Ni opposition 4 thereto. Furthermore, since Ni did not  
18 meet its burden of proof as discussed in our denial of Ni substantive motion 3, we  
19 did not reach Ni reply 3. Similarly, as discussed in our denial of the relevant  
20 portions of Rauch substantive motions 1 and 3, since Rauch did not meet its  
21 burden of proof as movant, we did not reach Ni oppositions 1 and 3 thereto.  
22 Likewise, as discussed in our granting of the relevant portions of Rauch

1 substantive motions 1 and 3, we credited the testimony of Dr. Cheng and did not  
2 rely upon the direct testimony of Dr. Badley to Rauch's detriment.

3 Based on the foregoing, Rauch substantive motion 5 is **dismissed** as  
4 moot since we have not relied upon any of the objected to testimony sought to be  
5 excluded to Rauch's detriment.

6 **XI. Ni Miscellaneous Motion 4**

7 Pursuant to 37 CFR § 1.155(c), Ni seeks to exclude from evidence:

8 (a) exhibits related to Rauch's priority statements in (i) related interference  
9 105,240 (RX 1074), (ii) this interference (RX 1025, RX 1038, RX 1052 and RX  
10 1054)<sup>15</sup> and (iii) related interference 105,380 (RX 1051);

11 (b) direct (RX 1074) and deposition (NX 2179-2181) testimony of Dr. Gavin  
12 R. Screanton in related interference 105,240;

13 (c) direct testimony of Norman Boiani (RX 1075); and,

14 (d) selected portions of the redirect testimony of Dr. Cheng (NX 2124, p.  
15 132, l. 16 - p. 135, l. 5 and p. 135, l. 9 - p. 136, l. 13) (Paper 86, pp. 1-2). Rauch  
16 opposes (Paper 80); Ni replies (Paper 88).

17 Ni contends (Paper 86, pp. 22-23) that

18 RX 1025, RX 1038, RX 1051, RX 1052 and RX 1054  
19 should be excluded under FRE 901 for lack of  
20 authentication and lack of foundation. In addition,  
21 these exhibits should be excluded under FRE 1001  
22 (4), 1002, and 1003, *inter alia*, because none of these  
23 exhibits appear to be originals nor admissible  
24 duplicates of the originals. Furthermore, these  
25 exhibits should be excluded under FRE 403, *inter alia*,  
26 because its [sic] probative value, if any, is outweighed

---

<sup>15</sup> Exhibits RX 1025 and RX 1038 are also relied upon in Rauch's priority statement in related interference 105,240.

1 by considerations of waste of time, lack of  
2 authentication and the reliability of the copies.

3 Furthermore, RX 1074, the declaration of Dr.  
4 Gavin R. Screaton, should be excluded under FRE  
5 403 because its probative value, if any, is far  
6 outweighed by confusion of the issues. In addition,  
7 RX 1074 should be excluded under 37 C.F.R.  
8 § 41.122(b) because the declaration does not  
9 respond to arguments raised in an opposition but  
10 merely is an attempt by Rauch to make additional  
11 arguments in a reply that should have been raised in  
12 a motion. Furthermore, contingent upon the Board  
13 excluding RX 1074, Party Ni moves to exclude NX  
14 2179, NX 2180 and NX 2181 for being irrelevant  
15 under FRE 401 and confusing the issues under FRE  
16 403.

17 In addition, Party Ni moves to exclude RX  
18 1075, the Declaration of Norman Boiani, under FRE  
19 1002 because Exhibit A appears to be a photocopy,  
20 not an original, of a laboratory notebook page.  
21 Furthermore, Party Ni moves to exclude RX 1075  
22 under FRE 403 because Exhibit A of RX 1075 is  
23 taken out of context of the rest of the laboratory  
24 notebook. Party Ni's inability to determine the context  
25 of Exhibit A is unfairly prejudicial and this prejudice far  
26 outweighs any probative value of RX 1075.

27 Lastly, the above-cited portions of NX 2124  
28 should be excluded under FRE 611(c), FRE 403, and  
29 Cross Examination Guideline [3] of the Standing  
30 Order. The leading questions asked by Rauch's  
31 counsel clearly suggested single answers to the  
32 witness which resulted in the interjection of the  
33 opinions of counsel for Rauch in place of Dr. Cheng's  
34 opinions. Clearly the prejudicial effect of such  
35 testimony far outweighs its probative value, and the  
36 above-cited evidence should be excluded or, at most,  
37 accorded little weight by the Board.

38 Ni's motion has serious procedural defects. Rule 155(c) provides that a  
39 motion to exclude evidence must explain the objections and identify the  
40 objections in the record. As explained in Standing Order ¶ 21.3(a) a motion to

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 69  
Paper 101

1 exclude evidence shall (1) identify where in the record the objection was  
2 originally made and (2) identify where in the record the evidence was relied upon  
3 by the opponent, and (3) address objections to exhibits (in whole or in part) in  
4 exhibit numerical order. According to Standing Order § 21.1, the objection to the  
5 admissibility of evidence should be filed as part of a motion to exclude the  
6 evidence.

7 First, Ni contends that it timely objected to exhibits RX 1025, RX 1038, RX  
8 1051, RX 1052 and RX 1054 as shown in exhibits NX 2194 and NX 2195, filed in  
9 support of its motion.

10 127. Ni exhibits NX 2194 and NX 2195 are "REDACTED" papers entitled  
11 "NI OBJECTIONS TO THE ADMISSIBILITY OF RAUCH'S SUPPLEMENT  
12 EXHIBIT 1054 AND RAUCH'S RESPONSES TO NI'S OBJECTIONS TO  
13 EXHIBITS AND 1050-1052" and "NI OBJECTIONS TO THE  
14 ADMISSIBILITY OF RAUCH EXHIBITS 1050, 1051 AND 1052,"  
15 respectively.

16 128. Ni has not provided evidence that it timely objected to exhibits RX  
17 1025 and RX 1038.

18 129. Ni has not identified where in the record exhibits RX 1025, RX  
19 1038, RX 1051, RX 1052, RX 1054 and RX 1075 were relied upon by  
20 Rauch.

21 130. According to Ni, RX 1074 and NX 2124 were relied upon in Rauch  
22 replies 1, 3 and 4 (Paper 86, p. 6, ¶ 3 and p. 7, ¶ 1).

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 70  
Paper 101

1       131.       Rauch's exhibit list (Paper 93, p. 7) identifies exhibit RX 1051 as a  
2       document upon which Rauch will rely to prove its earliest corroborated  
3       conception of the subject matter of the count in related interference  
4       105,380.

5       132.       Similarly, Rauch's exhibit list (Paper 93, p. 10) identifies exhibit RX  
6       1074 as the declaration of Dr. Gavin R. Screanton filed in related  
7       interference 105,240.

8       Thus, the deposition testimony of Dr. Screanton (NX 2179-2181) is part of  
9       related interference 105,240, not this interference. Indeed, Ni's motion to  
10      exclude NX 2179-2181 is expressly contingent upon the Board excluding Dr.  
11      Screanton's direct testimony (RX 1074) (Paper 86, p. 22).

12      133.       Ni admits that Rauch has not relied on any testimony from Norman  
13      Boiani to date in this interference (Paper 86, p. 6, ¶ 4).

14      Thus, Ni has failed to object timely to evidence it seeks to exclude (RX 1025  
15      and RX 1038). Furthermore, Ni is seeking to exclude evidence which is either  
16      not of record in this interference (RX 1051, RX 1074, NX 2179-2181 and RX  
17      1075<sup>16</sup>) and/or has not been relied upon by Rauch in this interference (RX 1075).

18      Therefore, Ni miscellaneous motion 4 to exclude evidence is **denied** as to  
19      exhibits RX 1025, RX 1038, RX 1051, RX 1074, NX 2179-2181 and RX 1075.

20      134.       Exhibits RX 1025, RX 1038, RX 1052 and RX 1054 are identified  
21      as documents said to prove Rauch's earliest corroborated date of

---

<sup>16</sup> Rauch's Exhibit List explicitly states that exhibit RX 1075 is "**WITHHELD**" in this interference (Paper 93, p. 10, original emphasis).

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 71  
Paper 101

1 conception of the subject matter of the count in this interference (Paper  
2 93, pp. 4, 5 and 7).

3 According to 37 CFR § 41.204(a)(2)(iv), a party filing a priority statement  
4 must "[p]rovide a copy of the earliest document upon which the party will rely to  
5 show conception." Exhibits RX 1025, RX 1038, RX 1052 and RX 1054 were  
6 served by Rauch in fulfillment of the requirement (FF 133). Ni does not contend  
7 that Rauch has relied on any of exhibits RX 1025, RX 1038, RX 1052 and RX  
8 1054 in support of any of Rauch's motion/opposition/reply papers. The time for  
9 Rauch to lay a foundation for and authenticate its exhibits RX 1025, RX 1038, RX  
10 1052 and RX 1054 is when Rauch relies upon them, i.e., as part of its priority  
11 motion. The time for us to weigh the reliability and probative value of exhibits RX  
12 1025, RX 1038, RX 1052 and RX 1054 is when they are submitted as evidence  
13 as part of Rauch's priority motion when the priority motion is filed. Therefore, Ni  
14 miscellaneous motion 4 to exclude evidence is **denied** as to exhibits RX 1025,  
15 RX 1038, RX 1052 and RX 1054.

16 As to the last evidence at issue, selected portions of the deposition  
17 testimony of Dr. Cheng (NX 2124, p. 132, l. 16 - p. 135, l. 5 and p. 135, l. 9 - p.  
18 136, l. 13), Ni contends that Rauch relied on the deposition testimony of Dr.  
19 Cheng in Rauch replies 1, 3 and 4 (Paper 86, p. 7, ¶ 1).

20 135. Ni explicitly directs our attention (Paper 86, pp. 17-18) to the  
21 following testimony as an example of how the redirect testimony of Dr.  
22 Cheng violates FRE 611(c), FRE 403 and Cross Examination Guideline  
23 [3]:

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 72  
Paper 101

1 MR. WISE: Okay. Back on the record.

2 Q. I want to have you focus on paragraph 10.  
3 Paragraph 10 you said, "The specification of the '861  
4 application also contains additional substantial  
5 disclosure regarding antibodies to TRAIL-R, including  
6 methods for obtaining these antibodies and methods  
7 of obtaining antigen binding fragments of these  
8 antibodies."

9 And it says "'861 application, page 13, line 14 to page  
10 15, line 6."

11 Where in the specification of the '861 application  
12 would you find additional substantial disclosure  
13 relating to the antibodies for TRAIL-R?

14 A. You mean where I can find the information?

15 Q. Yes.

16 A. That's indicated here is the page 13 and the line  
17 14 to 15, line 14 through page 15 of line 6.

18 Q. Okay. Can you direct me to that, please.

19 A. Where is the --

20 Q. You have that there. You were looking at the  
21 claims and you were going to show me support and  
22 specification.

23 MR. GOLDSTEIN: Objection.

24 THE WITNESS: So it's indeed in the page is 13,  
25 there is a title, "Antibodies" section, and talking about  
26 how antibody generated, including the monoclonal  
27 and polyclone antibodies.

28 MR. GOLDSTEIN: I am going to move to strike the  
29 question and the answer.

30 First, since Rauch responsive motion 4 was dismissed as moot, we did not  
31 reach Rauch reply 4. Second, Ni did not explain where and how Rauch relied  
32 upon the objected to portions of Dr. Cheng's redirect testimony in Rauch replies 1

1 and 3 to support its position. For example, how did Rauch rely upon this  
2 allegedly elicited testimony to support its motion 1 for benefit of the filing date of  
3 an earlier application for the subject matter of a count directed to a genus of  
4 functional proteins, i.e., purified TRAIL-R polypeptides having an amino acid  
5 sequence that is at least 90% identical to SEQ ID NO:2 of Rauch's involved '358  
6 patent, wherein the polypeptides bind TRAIL. Third, to the extent Ni argues that  
7 the objected to portions of Dr. Cheng's redirect testimony are irrelevant,  
8 confusing or prejudicial, that objection goes to the weight to be accorded the  
9 testimony, not its admissibility. We have accorded Dr. Cheng's testimony the  
10 weight appropriate to its relevance and the underlying facts and data relied upon  
11 in support of his opinion. Ni has not shown otherwise. Therefore, Ni  
12 miscellaneous motion 4 to exclude evidence is **denied** as to the selected  
13 portions of the redirect deposition testimony of Dr. Cheng (NX 2124, p. 132, l. 16  
14 - p. 135, l. 5 and p. 135, l. 9 - p. 136, l. 13).

15 Based on the foregoing, Ni miscellaneous motion 5 is **denied**.

16 **XII. Order**

17 Based on the foregoing and for the reasons given, it is

18 ORDERED that Ni substantive motion 1 to substitute Ni proposed count 2  
19 for current Count 1 is **denied**;

20 FURTHER ORDERED that Ni substantive motion 2 for benefit for the  
21 purpose of priority is **dismissed** as moot as to Ni proposed count 2, **granted** as  
22 to the 29 July 1997 filing date of the 60/054,021 application for Count 1 and  
23 otherwise **denied**;

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 74  
Paper 101

1           FURTHER ORDERED that Ni substantive motion 3 seeking judgment that  
2   all Rauch's involved claims are unpatentable under 35 U.S.C. § 102(e) as  
3   anticipated by U.S. Patent 6,872,568 is **denied**;

4           FURTHER ORDERED that Ni miscellaneous motion 4 to exclude certain  
5   evidence is **denied**;

6           FURTHER ORDERED that Rauch substantive motion 1 for benefit for the  
7   purpose of priority as to Count 1 is **granted** as to the 28 March 1997 and 4 June  
8   1997 filing dates of applications 08/829,536 and 08/869,852, respectively, and  
9   otherwise **denied**;

10          FURTHER ORDERED that Rauch substantive motion 2 to designate Ni  
11   claims 46, 55, 63, 64, 110 and 118 as corresponding to Count 1 is **denied**;

12          FURTHER ORDERED that Rauch substantive motion 3 is **granted** to the  
13   extent that Ni claims 35, 36, 38-45, 47-54, 56-61, 75, 83, 92, 99, 100, 102-109,  
14   111-116, 127-133, 168-178 and 180-203 are unpatentable under 35 U.S.C.  
15   § 102(e) as anticipated by U.S. Patent 6,072,047, **moot** as to anticipation under  
16   § 102(e) by U.S. Patents 6,642,358 and 6,569,642, and otherwise **denied**;

17          FURTHER ORDERED that Rauch responsive motion 4 is **dismissed** as  
18   moot in view of the denial of Ni substantive motion 1; and,

19          FURTHER ORDERED that Rauch miscellaneous motion 5 to exclude  
20   certain evidence is **dismissed** as moot.

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 75  
Paper 101

_____	)	
RICHARD E. SCHAFER	)	
Administrative Patent Judge	)	
	)	
	)	
_____	)	BOARD OF PATENT
ADRIENE LEPIANE HANLON	)	APPEALS AND
Administrative Patent Judge	)	INTERFERENCES
	)	
	)	
_____	)	
CAROL A. SPIEGEL	)	
Administrative Patent Judge	)	

Enc: MOLECULAR BIOLOGY AND BIOTECHNOLOGY, R. Meyers, ed., VCH Publishers, Inc.,  
New York, NY (1985), p . 860

MOLECULAR CELL BIOLOGY, second edition, Darnell et al., W.H. Freeman and  
Company, New York, NY (1990), pp. 44-48.

MICROBIOLOGY: An Introduction, Tortora et al., The Benjamin/Cummings Publishing  
Company, Inc., Menlo Park, California, (1982) pp. 111-112, copy enclosed; MCB, pp. 55-  
65.

CLINICAL DIAGNOSIS AND MANAGEMENT BY LABORATORY METHODS, sixteenth  
edition, J. B. Henry ed., W.B. Saunders Company, Philadelphia (1979), Vol. I, p. 992.

Letter Brief  
Ex. C  
D-M

Interference No. 105,381  
Human Genome Sciences, Inc. (Ni) v. Immunex Corp. (Rauch)

Page 76  
Paper 101

cc (overnight delivery)

Counsel for HUMAN GENOME SCIENCES, INC.:

Jorge A. Goldstein, Esq.  
STERNE, KESSLER, GOLDSTEIN & FOX PPLC  
1100 New York Avenue, N.W.  
Washington, DC 20005-3934  
Tel: 202-371-2600  
Fax: 202-371-2540

Counsel for IMMUNEX CORPORATION:

Michael J. Wise, Esq.  
PERKINS COIE LLP  
1620 26th Street  
6th Floor, South Tower  
Santa Monica, CA 90404-4013  
Tel: 310-788-3210  
Fax: 310-788-3399

Attorney for GENENTECH (Interference 105361):

Oliver R. Ashe, Jr., Esq.  
ASHE, P.C.  
11440 Isaac Newton Sq. North  
Suite 210  
Reston, VA 20190  
Tel: 703-467-9001  
Fax: 703-467-9002

Letter Brief  
Ex. C  
D-M

# Molecular Biology and Biotechnology

## A Comprehensive Desk Reference

*Edited by*  
**Robert A. Meyers**



Letter Brief  
Ex. C  
D-M

Robert A. Meyers, Ph.D.  
3715 Gleneagles Drive  
Tarzana, CA 91356, USA

*Management Supervised by:*  
Chernow Editorial Services, Inc.,  
1133 Broadway, Suite 721, New York, NY, USA

*Cover design by:* G & H SOHO, Inc.

Cover art courtesy of Dr. Alexander Wlodawer from Figure 1 of his article,  
"AIDS, Inhibitor Complexes of HIV-1 Protease in."  
Art prepared by Dr. Jacek Lubkowski.

Library of Congress Cataloging-in-Publication Data

Molecular biology and biotechnology : a comprehensive desk reference /  
Robert A. Meyers, editor.

p. cm.

Includes bibliographical references and index.

ISBN 1-56081-569-8 (alk. paper). — ISBN 1-56081-925-1 (pbk.: alk. paper)

1. Molecular biology—Encyclopedias. 2. Biotechnology—Encyclopedias.

I. Meyers, Robert A. (Robert Allen), 1936–

QH506.M66155 1995

574.8'8'03—dc20

95-9063

CIP

© 1995 VCH Publishers, Inc.

This work is subject to copyright.

All rights are reserved, whether the whole or part of the material is concerned,  
specifically those of translation, reprinting, re-use of illustrations, broadcasting,  
reproduction by photocopying machine or similar means, and storage in data  
banks.

Registered names, trademarks, etc. used in this book, even when not specifically  
marked as such, are not considered to be unprotected by law.

Printed in the United States of America

ISBN 1-56081-569-8 (hardcover)

Printing History:

10 9 8 7 6 5 4 3 2

ISBN 1-56081-925-1 (softcover)

Printing History:

10 9 8 7 6 5 4 3 2

Published jointly by:

VCH Publishers, Inc.  
220 East 23rd Street  
New York, NY 10010  
USA

VCH Verlagsgesellschaft mbH  
P.O. Box 10 11 61  
D-6940 Weinheim  
Federal Republic of Germany

VCH Publishers (UK) Ltd.  
8 Wellington Court  
Cambridge CB1 1HW  
United Kingdom

Fax: (212) 481-0897

E-mail address: order@vch.com

Letter Brief  
Ex. C –  
D-M

## 860 Sequence Analysis

Sequences of nucleic acids in DNA and RNA and of amino acids in proteins define the primary structure of these molecules. Sequence analysis is carried out using computer programs that implement algorithms to determine sequence properties and to compare sequences. Sequence comparison can indicate whether an RNA or protein molecule or region of DNA is already known (identity) or has some degree of similarity to a known sequence. Sequence similarity may indicate similar structure or function. Sequence analysis can suggest the function of an unknown sequence based on the features it contains. Sequence analysis is a necessary preliminary to detailed experimental studies of structure, function, and interactions of biological macromolecules. Sequences are the information repository of the cell and a natural index to our growing understanding of cellular processes as dynamic systems of interactions between macromolecules.

## 1 PURPOSE OF SEQUENCE ANALYSIS

### 1.1 PREDICTION OF FUNCTION

Sequences that are unlike any known sequence may still be made to yield information that can suggest their possible function. The function of nucleic acids and proteins depends on their structure and involves complex interactions in three dimensions. It is not presently understood whether it is possible, in general, to derive structure from sequence. Sequence alone is therefore often inadequate to determine function. Predictions made from sequence analysis need to be experimentally tested. Nevertheless, computer analysis of sequences is valuable in suggesting the most useful experiments to perform.

### 1.2 REVEALING SIMILARITY

The first thing to do with a newly determined sequence is to compare it with all known sequences. The outcome may show identity to a known sequence, which may prove disappointing if one is hoping for something new. Similarity to a known sequence may suggest something new that can be characterized with relatively little effort. A totally unknown sequence may be a frustrating result: considerable effort will be needed to understand its function.

Sequence comparison is a nontrivial pursuit, and both statistical and biological considerations are involved. Statistically significant similarities (under some model and at some chosen level of significance) may be biologically meaningless. Sequence motifs that are statistically nonsignificant in similarity may encode the same function (this is likely to occur because the statistical model based on sequence alone is incomplete). In an area fraught with such difficulties, common sense and interpretation based on utility are paramount.

Sequence dissimilarity can range from identity, difference due to sequencing errors, difference due to population polymorphism (individual variants), and differences in multiple copies of a gene in a single individual (multigene families) to wide evolutionary divergence of genes in different organisms. Sequences that are similar due to common function may not share a common ancestral sequence in biological evolution. In general, ideas about the evolutionary relationships of sequences are not experimentally testable. Sequence homology (similarity due to descent from a common ancestor) is a hypothesis, not an observable fact, except in the case of microbial populations with high mutation rates and short

generation times, which may be studied experimentally through time.

## 2 ANALYSIS OF SINGLE SEQUENCES

### 2.1 DNA COMPOSITION, ISOCHORES, AND CODON USAGE

Nucleotides in DNA sequences may be counted as singlets, doublets, or triplets in either strand. Doublets or triplets may be counted as overlapping or nonoverlapping in two or three phases, respectively, on either strand. The genomes of various organisms vary considerably in their DNA composition. Warm-blooded vertebrates have a higher G+C content, which correlates with the higher thermal stability of GC over AT base pairs. Composition of regions within a genome can also vary considerably. Mammalian genomes contain relatively GC-rich and AT-rich regions, which are called isochores. Overlapping doublet frequencies are highly characteristic for an organism. CG dinucleotides are less common than expected in vertebrates and angiosperms, probably because spontaneous deamination of 5-methylcytosine to thymine prevents the repair of methylated CpG. In DNA coding for protein, one phase of nonoverlapping triplets will be the phase of translation and the triplets will be codons. In a gene, the possible codons for each amino acid are unevenly used, and the frequency table for the 64 triplets is called codon usage. Codon usage is different between different species and between highly and lowly expressed gene in the same species.

### 2.2 MAPPING DNA SEQUENCE FEATURES

Mapping the position of features on a DNA sequence is an important step in investigating its function. It is easy to map sites that can be precisely defined, such as stop codons or restriction enzyme recognition sites. Once DNA has been sequenced, the sizes of the fragments produced with any enzyme can be readily calculated. Features such as promoters, splice junctions, and ribosome binding sites are very difficult to predict because they are hard to specify. Mapping is most simply achieved by comparing the probe sequence with each position of the DNA sequence in turn and noting the hits. More sophisticated algorithms exist for rapid searching in large problems.

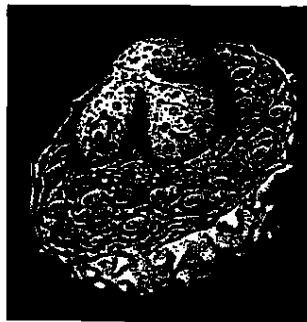
### 2.3 REPETITIVE SEQUENCES

Direct repeats and inverted repeats (sometimes called dyad symmetries) are common in DNA from many sources. Mammalian genomes contain families of long (LINE) and short (SINE) repeats. Repeats of *L1* (*Kpn* I) type are 5000 to 7000 bp long and are present in the genome in  $10^3$  to  $10^4$  copies. Repeats of *Alu* type are 350 bp long and occur in as many as  $9 \times 10^4$  copies. *Alu* repeats make human DNA hard to assemble from gel sequencing reads into the finished sequence. Inverted repeats occur in DNA coding for structural RNA, and these symmetry properties enable the RNA to fold into its secondary structure.

The dot plot is a diagram that reveals the presence of repeats and inverted repeats in sequences. It is also useful for comparing two different nucleic acid or protein sequences to detect regions of similarity. The dot plot is a rectangular array with rows labeled by one sequence and columns labeled by the other. A cell  $i, j$  can be used to represent the result of comparison of the  $j$ th residue of sequence A with the  $i$ th residue of sequence B. The simplest form of dot plot results from placing a diagonal mark in each cell where

# Molecular Cell Biology

SECOND EDITION



SCIENTIFIC & TECHNICAL  
INFORMATION CENTER

FEB 06 1994

PATENT & TRADEMARK OFFICE

JAMES DARNELL

*Vincent Astor Professor  
Rockefeller University*

▲

HARVEY LODISH

*Member of the Whitehead Institute for  
Biomedical Research  
Professor of Biology, Massachusetts  
Institute of Technology*

▲

DAVID BALTIMORE

*President  
Rockefeller University*

SCIENTIFIC  
AMERICAN  
BOOKS

Distributed by W. H. Freeman and Company, New York

Letter Brief  
Ex. C  
D-M

Cover illustration by Tomo Narashima

Library of Congress Cataloging-in-Publication Data

Darnell, James E.

Molecular cell biology / James Darnell, Harvey Lodish, David Baltimore.—2d ed.

p. cm.

Includes bibliographical references.

ISBN 0-7167-1981-9:—ISBN 0-7167-2078-7

(international student ed.):

I. Cytology. 2. Molecular biology. I. Lodish, Harvey F.  
II. Baltimore, David. III. Title.

[DNLM: 1. Cells. 2. Molecular Biology. QH 581.2 D223m]

QH581.2.D37 1990

574.87'6042—dc20

DNLM/DLC

for Library of Congress

89-70096

CIP

Copyright © 1990 by Scientific American Books, Inc.

No part of this book may be reproduced by any mechanical, photographic, or electronic process, or in the form of a phonographic recording, nor may it be stored in a retrieval system, transmitted, or otherwise copied for public or private use, without the written permission of the publisher.

Printed in the United States of America

Scientific American Books is a subsidiary of Scientific American, Inc. Distributed by W. H. Freeman and Company, 41 Madison Avenue, New York, New York 10010 and 20 Beaumont Street, Oxford OX1 2NQ England

5 6 7 8 9 0 KP 9 9 8 7 6 5 4 3

Letter Brief  
Ex. C  
D-M

## 44 CHAPTER 2 • MOLECULES IN CELLS

ent amino acids in proteins. Thus a 100-unit protein has  $20^{100}$  (more than  $10^{130}$ ) possible structures. This enormous variability means that cells and organisms can differ greatly in structure and function even though they are constructed of the same types of biopolymers produced by similar chemical reactions.

Starch (a storage form of glucose in plant cells), cellulose (a constituent of plant cell walls), and glycogen (a storage form of glucose in liver and muscle cells) are examples of another important type of biopolymer: the polysaccharide, which is built of sugar monomers (Figure 2-1). At least 15 different monomeric sugars can be bonded in multiple ways to form various polysaccharides; thus many polysaccharides are nonlinear, branched molecules.

Monomers are not the only small molecules important to cell structure. The lipids, for example, form the basic structure of cell membranes. Lipids cohere noncovalently in very large sheetlike complexes; the membranes thus formed are as crucial to living systems as are the biopolymers.

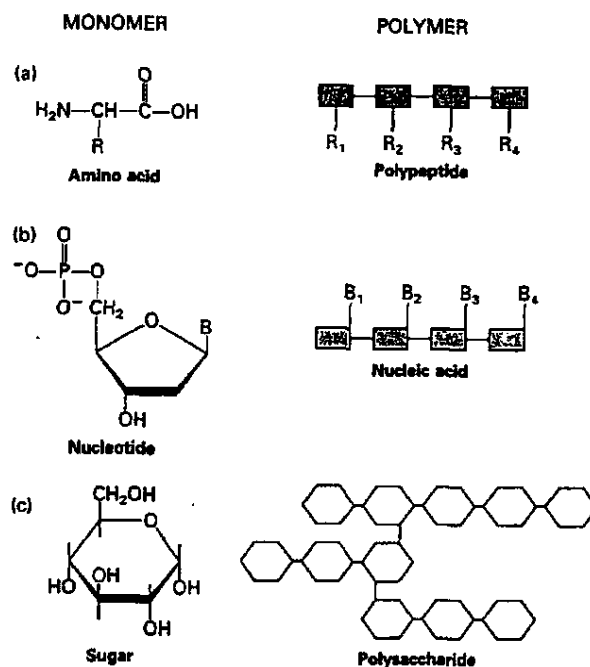
This chapter deals with the structures and some functions of biopolymers and small molecules; later chapters describe how the polymers are made and consider many of their other functions and interactions. ▲

## Proteins

Proteins are the working molecules of the cell. They catalyze an extraordinary range of chemical reactions, provide structural rigidity, control membrane permeability, regulate the concentrations of metabolites, recognize and noncovalently bind other biomolecules, cause motion, and control gene function. These incredibly diverse tasks are performed by molecules constructed from only 20 different amino acids.

### Amino Acids—the Building Blocks of Proteins—Differ Only in Their Side Chains

The monomers that make up proteins are called amino acids because, with one exception, each contains an amino group ( $-\text{NH}_2$ ) and an acidic carboxyl group ( $-\text{COOH}$ ). The exception, proline, has an imino group ( $-\text{NH}-$ ) instead of an amino group. At typical pH values in cells, the amino and carboxyl groups are ionized as  $-\text{NH}_3^+$  and  $-\text{COO}^-$ . All amino acids are constructed according to a basic design: a central carbon atom, called the  $\alpha$  carbon  $C_\alpha$  (because it is adjacent to the acidic carboxyl group), is bonded to an amino (or imino) group, to the carboxyl group, to a hydrogen atom, and to one variable group, called a side chain or R group (Figure 2-2). The side chains give the amino acids their individuality.



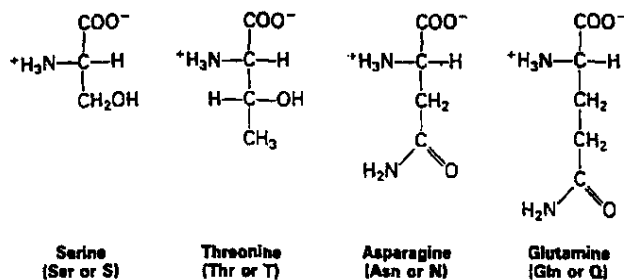
▲ **Figure 2-1** (a) Proteins, linear biopolymers called polypeptides, are formed from monomeric subunits termed amino acids. Each of the 20 different amino acids has a different R group, or side chain. Thus the polypeptide shown here, which is constructed of four amino acids, has  $20^4$ , or 160,000, possible structures. (b) Nucleic acids, also linear biopolymers, are formed from four monomers termed nucleotides, each of which has a different nitrogen-containing base structure (B). The nucleic acid shown here has  $4^4$ , or 256, possible structures. (c) Polysaccharides are built of monomeric saccharide (sugar) subunits. Because sugar residues can bind to one another at different positions, nonlinear branching polymers are often formed. The rings in (b) and (c) are depicted as Haworth projections (planar structures with a hint of perspective).

The amino acids represent the alphabet in which linear proteins are “written”; any student of biology must be familiar with the special properties of each letter of this alphabet. These letters can be classified into a few distinct categories.

The side chains of four of the amino acids are highly ionized and therefore charged at neutral pH. Arginine and lysine are positively charged; aspartic acid and glutamic acid are negatively charged and exist as aspartate and glutamate. The side chain of a fifth amino acid, histidine, is positively charged, but only weakly at neutral pH. In many cases, arginine may substitute for lysine, or aspartate for glutamate, with little effect on the structure or function of the protein.

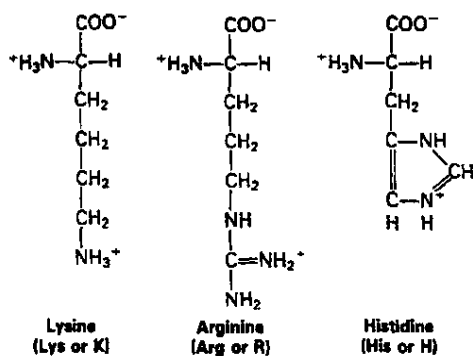
Serine and threonine, whose side chains have an  $-\text{OH}$  group, can interact strongly with water by forming hydrogen bonds. The side chains of asparagine and glutamine

## POLAR BUT UNCHARGED R GROUPS

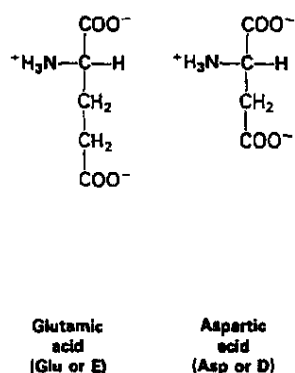


▼ **Figure 2-2** The structures of the 20 common amino acids. In each structure, a central carbon atom (the  $\alpha$  carbon) is bonded to an amino group (or to an imino group in proline), a carboxyl group, a hydrogen atom, and an R group. The R groups are in red.

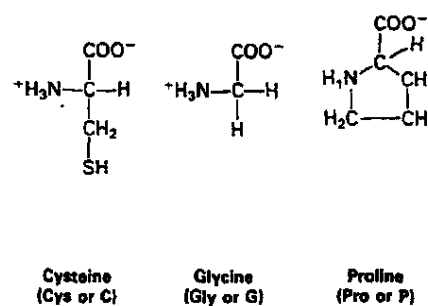
## POSITIVELY CHARGED R GROUPS



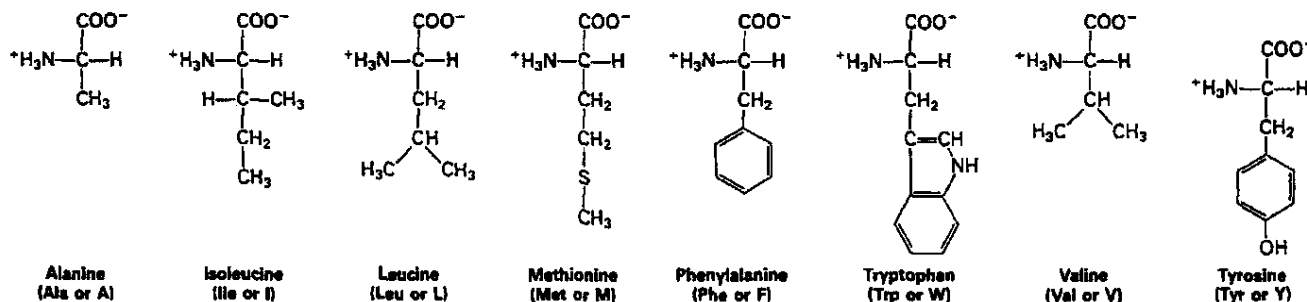
## NEGATIVELY CHARGED R GROUPS



## SPECIAL AMINO ACIDS



## HYDROPHOBIC R GROUPS



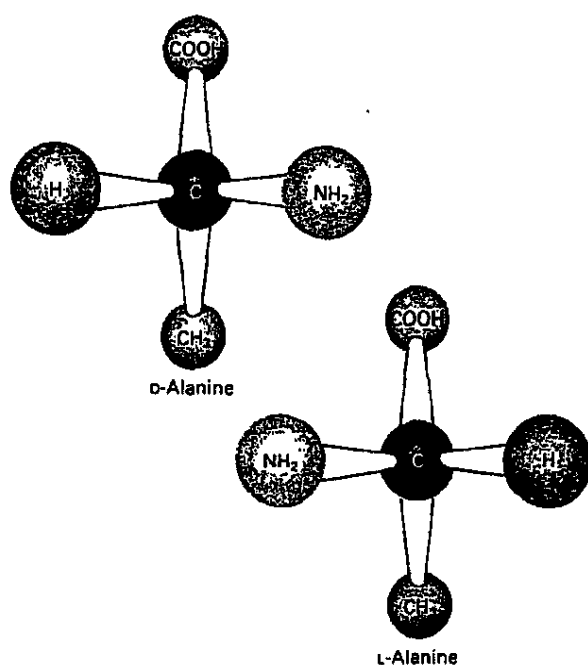
mine have polar amide groups with even more extensive hydrogen-bonding capacities. Together with the charged amino acids, these amino acids constitute the nine hydrophilic or polar amino acids.

The side chains of several other amino acids—alanine, isoleucine, leucine, methionine, phenylalanine, tryptophan, and valine—consist only of hydrocarbons, except for the sulfur atom in methionine and the nitrogen atom in tryptophan. These nonpolar amino acids are hydrophobic; their side chains are only slightly soluble in water. Tyrosine is also strongly hydrophobic because of its benzene ring, but its hydroxyl group allows it to interact with water, making its properties somewhat ambiguous.

Cysteine plays a special role in proteins because its  $-SH$  group allows it to dimerize through an  $-S-S-$  bond to a second cysteine, thus covalently linking regions of polypeptide to one another. When the  $-SH$  remains free, cysteine is quite hydrophobic.

Two other special amino acids are glycine and proline. Glycine has a hydrogen atom as its R group; thus it is the smallest amino acid and has no special hydrophobic or hydrophilic character. Proline, as an imino acid, is very rigid and creates a fixed kink in a polypeptide chain. It is quite hydrophobic.

The structure of all amino acids except glycine are asymmetrically arranged around the  $\alpha$  carbon, because it is bonded to four different atoms or groups of atoms

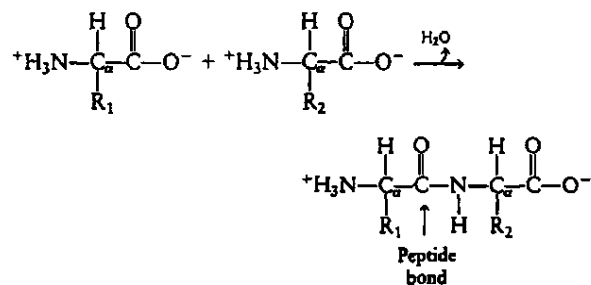


▲ **Figure 2-3** Stereoisomers of the amino acid alanine. The  $\alpha$  carbon is black.

( $-\text{NH}_2$ ,  $-\text{COOH}$ ,  $-\text{H}$ , and  $-\text{R}$ ). Thus all amino acids except glycine can have one of two stereoisomeric forms. By convention, these mirror-image structures are called the D and the L forms of the amino acid (Figure 2-3). They cannot be interconverted without breaking a chemical bond. With rare exceptions, only the L forms of amino acids are found in proteins.

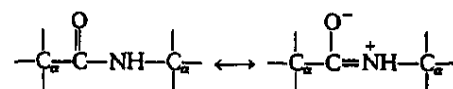
### Polypeptides Are Polymers Composed of Amino Acids Connected by Peptide Bonds

The *peptide bond*, the chemical bond that connects two amino acids in a polymer, is formed between the amino group of one amino acid and the carboxyl group of another. This reaction, called *condensation*, liberates a water molecule:



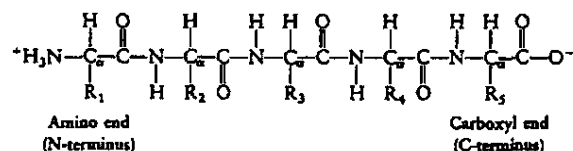
Because the carboxyl carbon and oxygen atoms are connected by a double bond, the peptide bond between car-

bon and nitrogen exhibits a partial double-bond character, as shown by the resonance structures



making it shorter than the typical C—N single bond. The six atoms of the peptide group (the two carbons of the adjacent amino acids and the carbon, oxygen, nitrogen, and hydrogen atoms of the bond) lie in the same plane (Figure 2-4a). However, adjacent peptide groups are not necessarily coplanar, due to rotation about the C—C $_\alpha$  and N—C $_\alpha$  bonds (Figure 2-4b).

A single linear array of amino acids connected by peptide bonds is called a *polypeptide*. If the polypeptide is short (fewer than 30 amino acids long), it may be called an *oligopeptide* or just a *peptide*. Polypeptides in living cells differ greatly in length; they generally contain between 40 and 1000 amino acids. Each polypeptide has a free amino group at one end (the N-terminus) and a free carboxyl group at the other (the C-terminus):

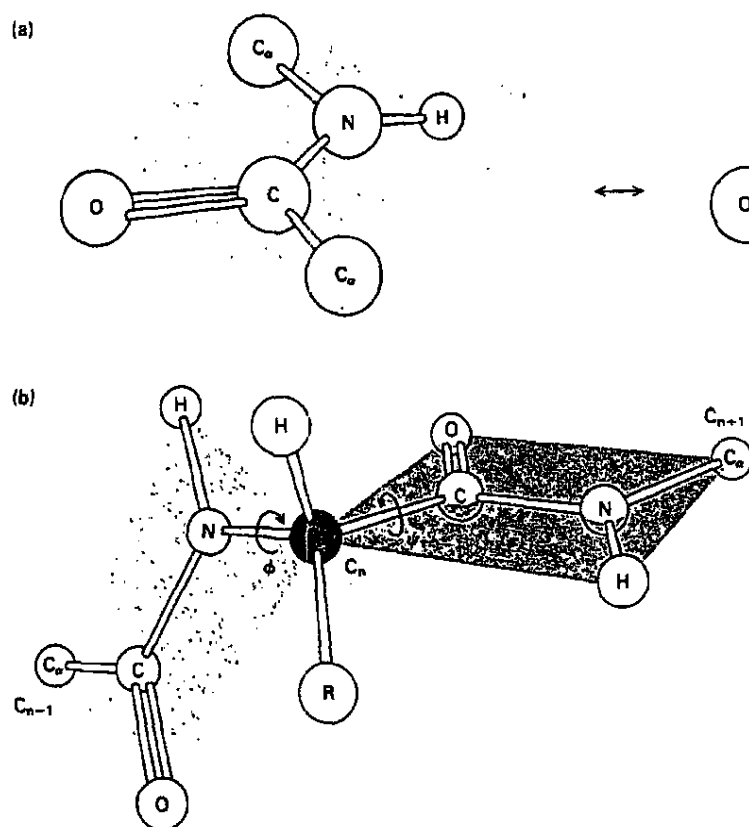


A protein is not merely a linear string of amino acids. The polypeptide folds up to form a specific three-dimensional structure that can be a long rod, as in the *fibrous proteins* that give tissues their rigidity, or a compact ball called a *globular protein*, as in many proteins that catalyze chemical reactions (enzymes), or a combination of balls and rods. The polypeptide can be modified further by the covalent or noncovalent attachment of additional small molecules.

A protein adopts a stable, folded conformation mainly through noncovalent (ionic, hydrogen, van der Waals, and hydrophobic) interactions. Its stability is also enhanced by the formation of covalent disulfide bonds between cysteines in different parts of the chain. Proteins may also consist of multiple polypeptide chains held together by noncovalent forces and, in some cases, by disulfide bonds. A well-characterized example is the hemoglobin molecule, which consists of four chains: two identical  $\alpha$  chains and two identical  $\beta$  chains (Figure 2-5).

### Three-dimensional Protein Structure Is Determined through X-ray Crystallography

The detailed three-dimensional structures of numerous proteins have been established by the painstaking efforts of many workers—notably, Max Perutz and John Kendrew, who perfected the x-ray crystallography of



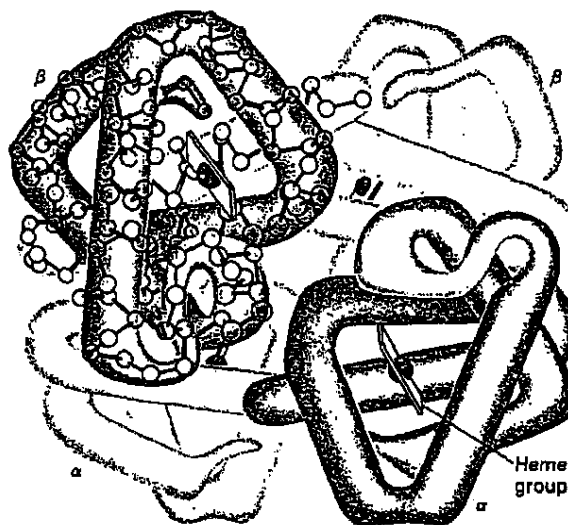
◀ **Figure 2-4** (a) Because the carbon-nitrogen peptide bond has a partial double-bond character, the peptide group is planar. (b) However, there is considerable flexibility in the geometry of polypeptides: rotation is possible about the two covalent single bonds that connect each  $\alpha$  carbon to the two adjacent planar peptide units. But some restrictions do apply to the values of  $\psi$  and  $\phi$ . For example, if the pictured adjacent peptide groups were coplanar, then certain oxygen and hydrogen atoms would be separated by less than their van der Waals radii and would repel one another.

proteins, in which beams of x-rays are passed through a crystal of protein. The wavelengths of x-rays are about 0.1–0.2 nanometers (nm)—short enough to resolve the atoms in the protein crystal. The three-dimensional structure of the protein can be deduced from the *diffraction pattern* of discrete spots that is produced when the scattered radiation is intercepted by photographic film. Such patterns are extremely complex; as many as 25,000 diffraction spots can be obtained from a small protein. Elaborate calculations and modifications of the protein (such as binding of heavy metal) must be made to interpret the diffraction pattern and to solve the structure of the protein.

Recently, three-dimensional structures of some small proteins have been determined by nuclear magnetic resonance (nmr) methods. An advantage of this approach is that it avoids the need to crystallize the protein. A disadvantage is that it is limited to relatively small proteins (up to about 20,000 molecular weight).

### The Structure of a Polypeptide Can Be Described at Four Levels

The structures adopted by polypeptides can be divided into four levels of organization. *Primary structure* refers to the linear arrangement of amino acid residues along a



▲ **Figure 2-5** The conformations assumed by the two  $\alpha$  and two  $\beta$  chains in a molecule of hemoglobin. Each chain forms several  $\alpha$  helices (see Figure 2-6). Only the backbones formed by the carbon and nitrogen atoms of the chains are shown here. A multitude of noncovalent interactions stabilize the conformations of the individual chains and the contacts between them. A heme group is bound to each chain. After R. E. Dickerson and I. Geis, 1969, *The Structure and Action of Proteins*, Benjamin-Cummings, p. 56. Copyright 1969 by Irving Geis.

polypeptide chain and to the locations of covalent bonds (mainly —S—S— bonds) between chains. *Secondary structure* pertains to the folding of parts of these chains into regular structures, such as  $\alpha$  helices and  $\beta$  pleated sheets. *Tertiary structure* includes the folding of regions between  $\alpha$  helices and  $\beta$  pleated sheets, as well as the combination of these secondary features into compact shapes (domains). *Quaternary structure* refers to the organization of several polypeptide chains into a single protein molecule, such as in hemoglobin.

### Two Regular Secondary Structures Are Particularly Important

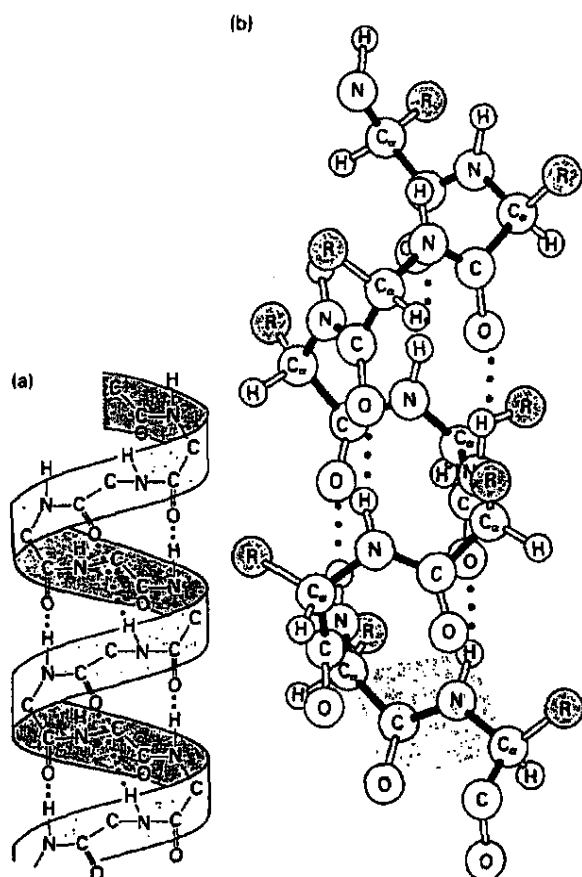
**The  $\alpha$  Helix** Although some regions of proteins are held in unique and irregular conformations, much protein structure involves repeated use of a limited number of regular configurations. One common structure, the  $\alpha$  helix, was first described by Linus Pauling and Robert B. Corey in 1951. Through careful model building, these scientists came to realize that polypeptide seg-

ments composed of certain amino acids tend to arrange themselves in regular helical conformations. In an  $\alpha$  helix, the carboxyl oxygen of each peptide bond is hydrogen-bonded to the hydrogen on the amino group of the fourth amino acid away (Figure 2-6), so that the helix has 3.6 amino acids per turn. Each amino acid residue represents an advance of about 1.5 Å along the axis of the helix. Every C=O and N—H group in the peptide bonds participates in a hydrogen bond, and the rigid planarity of the peptide bonds contributes to the rigid shape of the helix. In this inflexible, stable arrangement of amino acids, the side chains are positioned along the outside of a cylinder. The hydrogen-bonding potential of the peptide bonds is entirely satisfied internally, so that the polar or nonpolar quality of the cylindrical surface is determined entirely by the side chains. At least some of the amino acids in most proteins are organized into  $\alpha$  helices.

Certain amino acid sequences adopt the  $\alpha$ -helical conformation more readily than others. What determines this propensity is complicated, but some simple factors are evident. For instance, proline is rarely found in  $\alpha$ -helical regions because it cannot use its peptide nitrogen to make a hydrogen bond. Glycine also is an infrequent participant. Another inhibiting factor can be the tendency of multiple identically charged residues to repel each other.

The  $\alpha$  helix is a rodlike element of protein structure that serves many functions. A globular protein can be made up of short  $\alpha$ -helical rods connected by bends that allow the rods to interact with each other; hemoglobin, for instance, is 70 percent  $\alpha$  helical (see Figure 2-5). Alternatively, a single rod can span a long distance, as in the protein on the surface of the influenza virus (Figure 2-7a). Even in extended molecules, a, b, c the  $\alpha$  helix is usually found packed against other elements of protein, not as an isolated structure. Long fibers, such as the skin protein keratin or the muscle protein myosin (Figure 2-7b), can be formed by two or three  $\alpha$  helices that wrap gently around each other to form *coiled coils*. Small rods of  $\alpha$  helix interact with DNA in some DNA-binding proteins (Figure 2-7c). A helical rod bearing only hydrophobic side chains can span lipid membranes well because the hydrophilic peptide bonds are buried inside the helix.

Many  $\alpha$  helices are *amphipathic*: they expose hydrophilic side chains on one face and hydrophobic side chains on another face. Looking down the central axis of an  $\alpha$  helix (Figure 2-8a), the amino acid residues are arranged in a wheel; if the helix is amphipathic, most or all



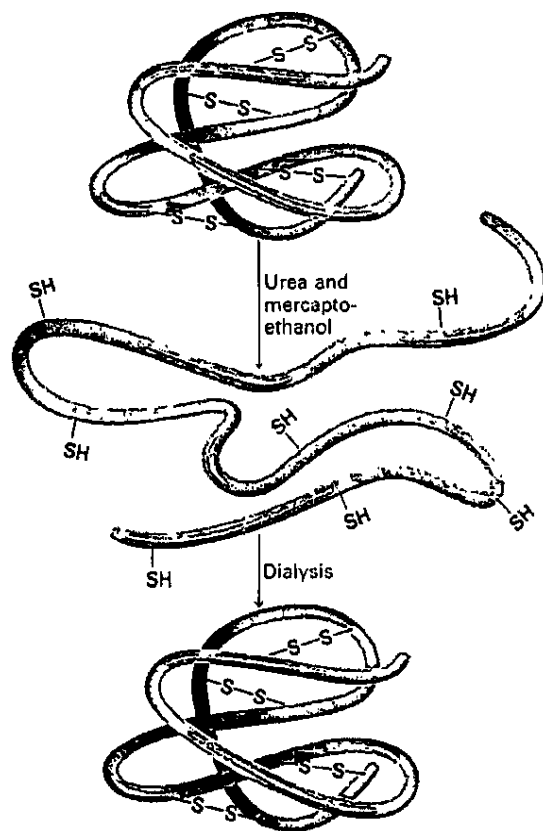
◀ **Figure 2-6** Models of the  $\alpha$  helix. (a) This ribbonlike representation without R groups emphasizes the helical form. (b) This ball-and-stick representation emphasizes the role of the individual atoms and shows the R groups (green) that protrude from the helix body at regular intervals. Some of the planes of the  $C_{\alpha}$ —CO—NH groups are shaded orange. Part (b) after L. Stryer, 1988, *Biochemistry*, 3d ed., W. H. Freeman and Company, p. 26.

valently bound prosthetic group. For example, staphylococcal nuclease—a bacterial enzyme of 149 residues that degrades DNA and RNA—is totally denatured in acid but renatures to its native conformation within 0.1 s after the solution is neutralized. The three-dimensional architecture of this protein is solely a consequence of interactions among its amino acids and with its aqueous environment. In such cases, the genetic program of the cell must only define the primary structure of the protein—the amino acid sequence—and the tertiary structure is assured. With care, most proteins can be carried through a denaturation-renaturation cycle. Thus it is generally true that linear structure determines three-dimensional architecture.

The native form of some proteins is not the conformation with the lowest free energy and consequently cannot be completely restored on renaturation. This is particu-

larly true of multichain proteins. The two chains of insulin, for example, can be separated by a combination of reducing agents (to break the disulfide bridges) and concentrated solutions of such chemicals as urea (to disrupt hydrogen and hydrophobic bonds). When the insulin renatures in the presence of oxidizing agents that promote the formation of disulfide bridges, a number of stable multichain aggregates do form, but *native* insulin molecules make up only a minor proportion of them. In the others, the re-formed disulfide bridges connect inappropriate parts of the chain.

Insulin is formed by the partial proteolysis (breaking down) of proinsulin, its larger precursor (see Figure 2-13). Denatured proinsulin, as opposed to the denatured two-chain form of insulin, can renature to form the native structure of proinsulin with a high efficiency. Presumably, within the cell, either proinsulin or preproinsulin folds in such a way that the correct disulfide bridges form at the lowest free energy. The cell utilizes these intermediate stages to form insulin, whose stable conformation is not the one of lowest free energy.



▲ **Figure 2-15** Denaturation and renaturation of a protein. Most polypeptides can be completely unfolded by treatment with an 8 M urea solution containing mercaptoethanol ( $\text{HSCH}_2\text{CH}_2\text{OH}$ ). The urea breaks intramolecular hydrogen and hydrophobic bonds, and the mercaptoethanol reduces each disulfide bridge to two  $-\text{SH}$  groups. When these chemicals are removed by dialysis, the  $-\text{SH}$  groups on the unfolded chain oxidize spontaneously to re-form disulfide bridges, and the polypeptide chain simultaneously refolds into its native configuration.

## Enzymes

Protein catalysts called *enzymes* are mediators of the dynamic events of life; almost every chemical reaction in a cell is catalyzed by an enzyme. Like other catalysts, enzymes increase the rates of reactions that are already energetically favorable; more precisely, enzymes increase the rates of forward and reverse reactions by the same factor. The name of an enzyme usually indicates its function: the suffix *-ase* is commonly appended to the name of the type of molecule on which the enzyme acts. Thus proteases degrade proteins, phosphatases remove phosphate residues, and ribonuclease cleaves RNA molecules.

The chemicals that undergo a change in a reaction catalyzed by an enzyme are the *substrates* of that enzyme. Because little free energy may be liberated in either direction in reversible reactions, the distinction between chemicals that are substrates and those that are products is often arbitrary.

Most enzymes are found inside cells, but a number are secreted by cells and function in the blood, the digestive tract, or other extracellular spaces. In microbial species, some enzymes function outside the organism. The number of different types of chemical reactions in any one cell is very large: an animal cell, for example, normally contains 1000–4000 different types of enzymes, each of which catalyzes a single chemical reaction or set of closely related reactions. Certain enzymes are found in the majority of cells because they catalyze common cellular reactions—the synthesis of proteins, nucleic acids, and phospholipids and the conversion of glucose and oxygen into carbon dioxide and water, which produces most of the chemical energy used in animal cells. Other enzymes are

Letter Brief  
Ex. C  
D-M

## 56 CHAPTER 2 • MOLECULES IN CELLS

found only in a particular type of cell within an organism, such as a liver cell or a nerve cell, because they carry out some chemical reaction unique to that cell. Also, many mature cells, including erythrocytes (red blood cells) and epidermal (skin) cells, may no longer be capable of making proteins or nucleic acids yet these cells still contain specific sets of enzymes that they synthesized at an earlier stage of differentiation.

### Certain Amino Acids in Enzymes Bind Substrates: Others Catalyze Reactions on the Bound Substrates

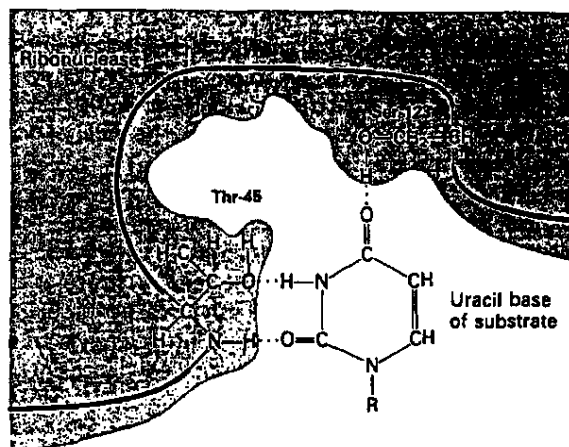
Two striking properties characterize all enzymes: their enormous *catalytic power* and their *specificity*. Quite often, the rate of an enzymatically catalyzed reaction is  $10^6$ – $10^{12}$  times that of an uncatalyzed reaction under otherwise similar conditions. The specificity of an enzyme is determined by the different rates at which it catalyzes closely similar chemical reactions or by its ability to distinguish between closely similar substrates.

Certain amino acid side chains of an enzyme are important in determining its specificity and its ability to accelerate the reaction rate. The properties of an enzyme are thus functions of its linear arrangement of amino acids and of the appropriate foldings of the peptide chain. Enzyme molecules have two important regions, or sites: one that recognizes and binds the substrate(s), and one that catalyzes the reaction once the substrate(s) have been bound. The amino acids in each of these key regions do not need to be adjacent in the linear polypeptide; they are brought into proximity in the folded molecule. In some enzymes, the catalytic site is part of the substrate-binding site. These two regions are called, collectively, the *active site*.

The binding of a substrate to an enzyme usually involves the formation of multiple noncovalent ionic, hydrogen, and hydrophobic bonds and van der Waals interactions (Figure 2-16). The array of chemical groups in the active site of the enzyme is precisely arranged so that the specific substrate can be more tightly bound than any other molecule (with the exception of some enzyme inhibitors) and the reaction can occur readily. In catalysis, covalent bonds between the enzyme and the substrate may be formed (and then broken) to reduce the activation energy for the reaction.

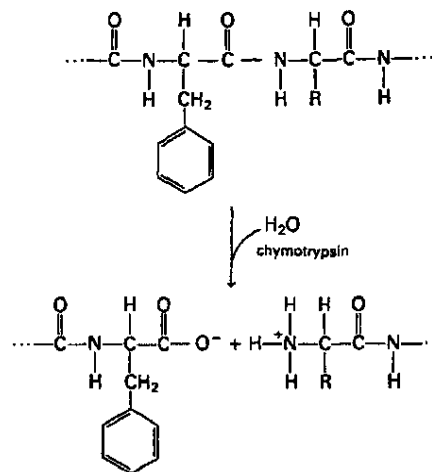
### Trypsin and Chymotrypsin Are Well-Characterized Proteolytic Enzymes

The proteolytic (protein-digesting) enzymes trypsin and chymotrypsin are synthesized in the pancreas and secreted into the small intestine as inactive precursors, or *zymogens*, called trypsinogen and chymotrypsinogen, respectively. These zymogens are not activated until they reach the small intestine where they hydrolyze peptide



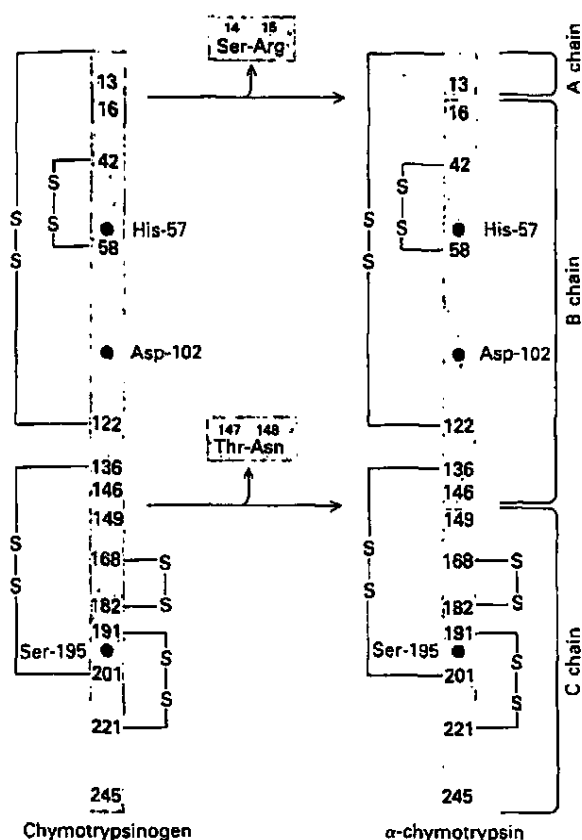
▲ **Figure 2-16** The specific binding of a substrate to an enzyme involves the formation of multiple noncovalent bonds. Here, two amino acid residues of the enzyme ribonuclease bind uracil, part of its substrate, by three hydrogen bonds. Substrates without the two C=O groups and one N—H group in the appropriate positions would be unable to bind or would bind less tightly. Other regions of the enzyme, not depicted here, bind other parts of the RNA substrate by hydrogen bonds and van der Waals interactions.

bonds of ingested proteins—a step in their digestion to single amino acids (Figure 2-17). The delay in activation serves an important regulatory purpose: it prevents the enzyme from digesting the pancreatic tissue in which it was made. Two irreversible proteolytic cleavages activate chymotrypsin. One cleavage removes serine 14 (the serine at position 14) and arginine 15 from chymotrypsinogen; the other removes threonine 147 and asparagine 148



▲ **Figure 2-17** The hydrolysis of a peptide bond by chymotrypsin.

Letter Brief  
Ex. C  
D-M



▲ **Figure 2-18** A linear representation of the conversion of chymotrypsinogen into chymotrypsin by the excision of two dipeptides. The positions of the disulfide bridges are indicated. In the folded molecule, histidine 57, aspartate 102, and serine 195 are located in the active site.

(Figure 2-18). Removal of these two dipeptides activates the protease function of the enzyme.

The hydrolysis of peptide bonds is energetically favorable ( $\Delta G^\circ = -2$  kcal/mol). Nonetheless, the activation energy for an *uncatalyzed* peptide-bond hydrolysis—say, in a neutral aqueous solution of a protein at room temperature—is so high that there is little or no hydrolysis even after several months. Biochemists can chemically hydrolyze proteins into their constituent amino acids by treating them with a 6 M solution of hydrochloric acid in an evacuated tube at 100°C for 24 h. Yet at 37°C and neutral pH, a molecule of trypsin or chymotrypsin can catalyze the hydrolysis of up to 100 peptide bonds per second. The power of enzymatically mediated catalysis is well-illustrated here: the addition of sufficient enzyme can do in seconds what otherwise would require harsh conditions and long times.

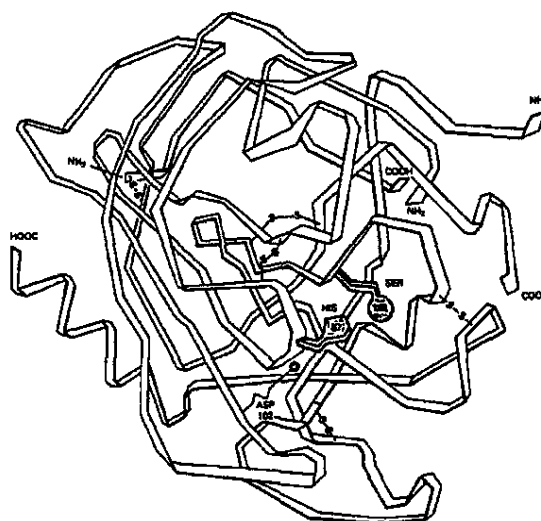
Chymotrypsin does not hydrolyze all peptide bonds; rather, it is selective for the peptide bond at the carboxyl ends of amino acids such as phenylalanine, tyrosine, and

tryptophan, which have large hydrophobic side chains. Trypsin, by contrast, is specific for the peptide bond on the C-terminal side of lysine and arginine residues.

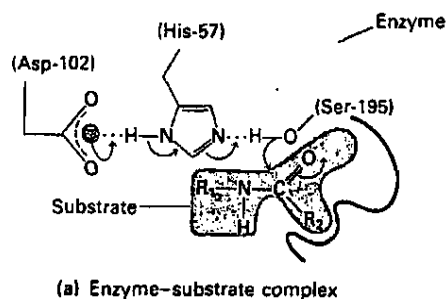
#### **Specific Amino Acid Side Chains of Chymotrypsin Aid in Substrate Binding**

The reaction mechanism of chymotrypsin was deduced, in part, from the three-dimensional structure obtained by x-ray crystallography (Figure 2-19). The enzyme contains three polypeptides—the A, B, and C chains, which have 13, 131, and 97 amino acids, respectively. These chains are interconnected by disulfide bridges (see Figures 2-18 and 2-19). The molecule has two key structural features: the active site and the *hydrophobic cleft* (a crevice bordered by the side chains of several hydrophobic amino acid residues), which serves as the binding site for specific amino acid residues on the substrate. The conformation of this pocket allows the residues lining it to participate in hydrophobic interactions with the large hydrophobic side chains of phenylalanine, tyrosine, or tryptophan. Neither charged side chains nor small hydrophobic residues on the substrate can make the noncovalent bonds necessary to fit into the cleft.

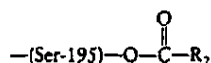
The hydrophobic residues of most globular proteins are buried in the interior; when such proteins are in their native states, the peptide bonds linking the hydrophobic residues are not accessible to hydrolysis by chymotrypsin. Normally, stomach acids (pH 1) denature ingested proteins so that proteases in that organ can partly degrade them before their exposure to further digestion by chymotrypsin at neutral pH in the intestine.



▲ **Figure 2-19** A three-dimensional model of  $\alpha$ -chymotrypsin determined from x-ray analysis. The N- and C-termini of the A, B, and C chains are indicated, as are the —S—S— bridges and the three amino acid residues of the active site (red). After B. W. Matthews et al., 1967, *Nature* 214:652.



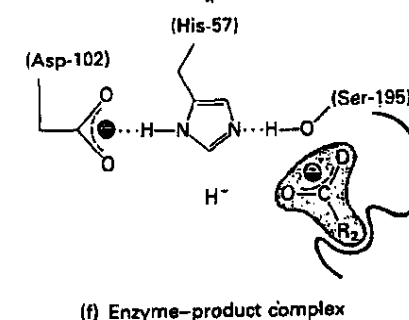
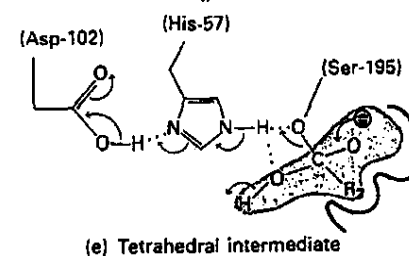
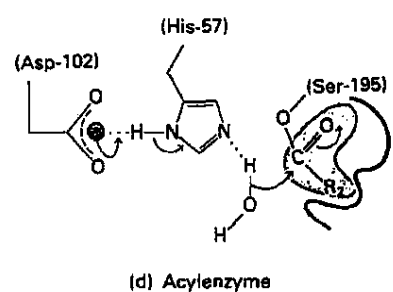
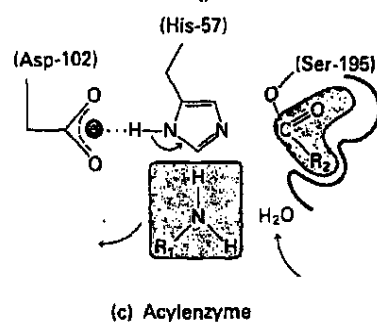
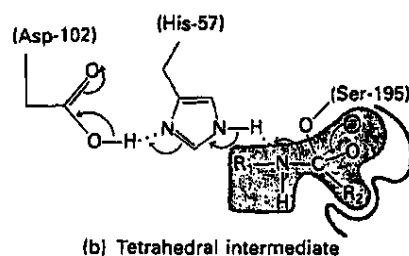
▲ **Figure 2-20** The mechanism of hydrolysis of a peptide bond by  $\alpha$ -chymotrypsin. Red curved arrows represent the movement of electrons. (a) The substrate is bound to the enzyme so that the bond to be hydrolyzed is positioned near serine 195. The negative charge (blue) surrounding the oxygens in aspartate 102 induces a charge relay system, which is initiated when the oxygen atoms on Asp-102 attract a proton from the nitrogen atom on His-57. When the negative charge reaches the second nitrogen in His-57, the nitrogen removes the proton from the hydroxyl group on Ser-195. The resulting  $O^-$  attacks the carbon of the bound substrate to form (b) a tetrahedral intermediate, so called because the carbon atom of interest temporarily has four single bonds. The hydrogen bound to the second nitrogen in His-57 is then added to the nitrogen of the substrate. As a result, the  $C-N$  bond of the substrate breaks, leaving (c)  $R_1NH_2$  and the acyl-enzyme intermediate



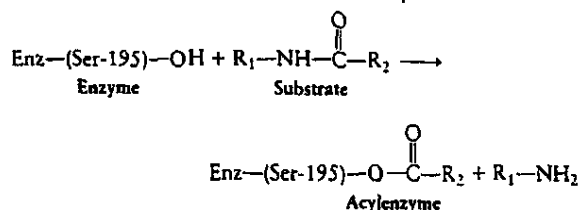
The  $R_1NH_2$  is discharged from the enzyme and replaced by water. In the resulting structure (d), a similar charge relay system is induced, and His-57 removes a proton from the hydrogen-bonded  $H_2O$ . The  $OH^-$  thus generated attacks the carbonyl carbon of the acyl-enzyme to form (e) another tetrahedral intermediate. The bond between the tetrahedral carbon and the oxygen of Ser-195 is hydrolyzed to yield (f)  $R_2COO^-$  bound noncovalently to the free enzyme, from which it is released. After R. M. Stroud, et al., 1975, in *Proteases and Biological Control*, E. Reich et al., eds. Cold Spring Harbor Laboratory, p. 25.

#### Other Amino Acid Side Chains of Chymotrypsin Have Roles in Catalyzing the Hydrolysis of the Bound Substrate

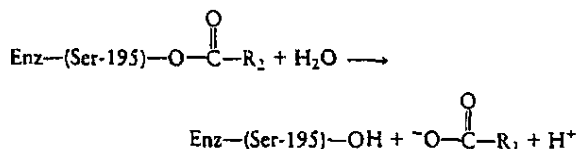
The catalytic activity of chymotrypsin depends on three amino acid residues: histidine 57, aspartate 102, and serine 195. These amino acids are distant from one another in the primary structure of the protein (see Figure 2-18), but the chains are folded in such a way in the active enzyme molecule that the three side chains are close together, in the correct position for catalyzing the hydrolysis of a peptide bond in a protein bound to the enzyme (see Figure 2-19). When chymotrypsinogen is proteolytically activated, the polypeptide conformation is altered to bring these three residues into correct alignment.



The hydrolysis reaction proceeds in two main steps. First, the peptide bond is broken and the carboxyl group is transferred to the hydroxyl residue of serine 195:



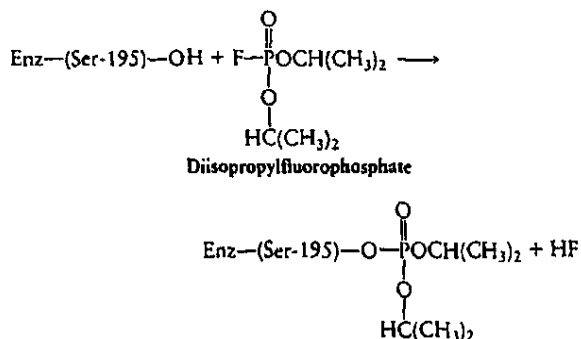
Second, this *acylenzyme* intermediate is hydrolyzed:



Note that the second step restores the enzyme to its original state.

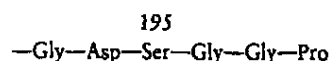
Aspartate 102 and histidine 57 facilitate the acylation reaction by removing the proton from serine 195 and adding it to the nitrogen of the departing amino group (Figure 2-20). In a similar manner, aspartate 102 and histidine 57 facilitate the hydrolysis of the acylenzyme. These enzymatically catalyzed steps—transfer of a proton from the enzyme to the substrate, formation of a covalent acylserine intermediate, and hydrolysis of the acylenzyme—all drastically reduce the overall activation energy of the proteolysis reaction.

The hydroxyl group on serine 195 is unusually reactive. The concept of an “active” serine residue at the active site predated the determination of the crystal structure of chymotrypsin. It was already known, for example, that the compound diisopropylfluorophosphate is a potent inhibitor of chymotrypsin; it reacts only with the hydroxyl on serine 195 to form a stable covalent compound that irreversibly inactivates the enzyme:



**Trypsin and Chymotrypsin Have Different Substrate-binding Sites** A comparison of trypsin and chymotrypsin will emphasize the nature of the specificity of enzymatically catalyzed reactions. About 40 percent of the amino acids in these two molecules are the same; in

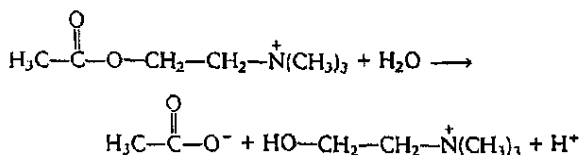
particular, the amino acid sequences in the vicinity of the key serine residue are identical:



The three-dimensional structures and catalytic mechanisms of these two enzymes are also quite similar, indicating that they evolved from a common polypeptide. The major difference between trypsin and chymotrypsin is found in the side chains of the amino acids that line the substrate-binding site. The negatively charged amino acids in this area of the trypsin molecule facilitate the binding of only positively charged (lysine or arginine) residues, instead of hydrophobic ones.

#### Other Hydrolytic Enzymes Contain Active Serine

Other, mostly unrelated, hydrolytic enzymes also contain an active serine residue that is essential for catalysis. For example, acetylcholinesterase catalyzes the hydrolysis of the neurotransmitter acetylcholine to acetate and choline:



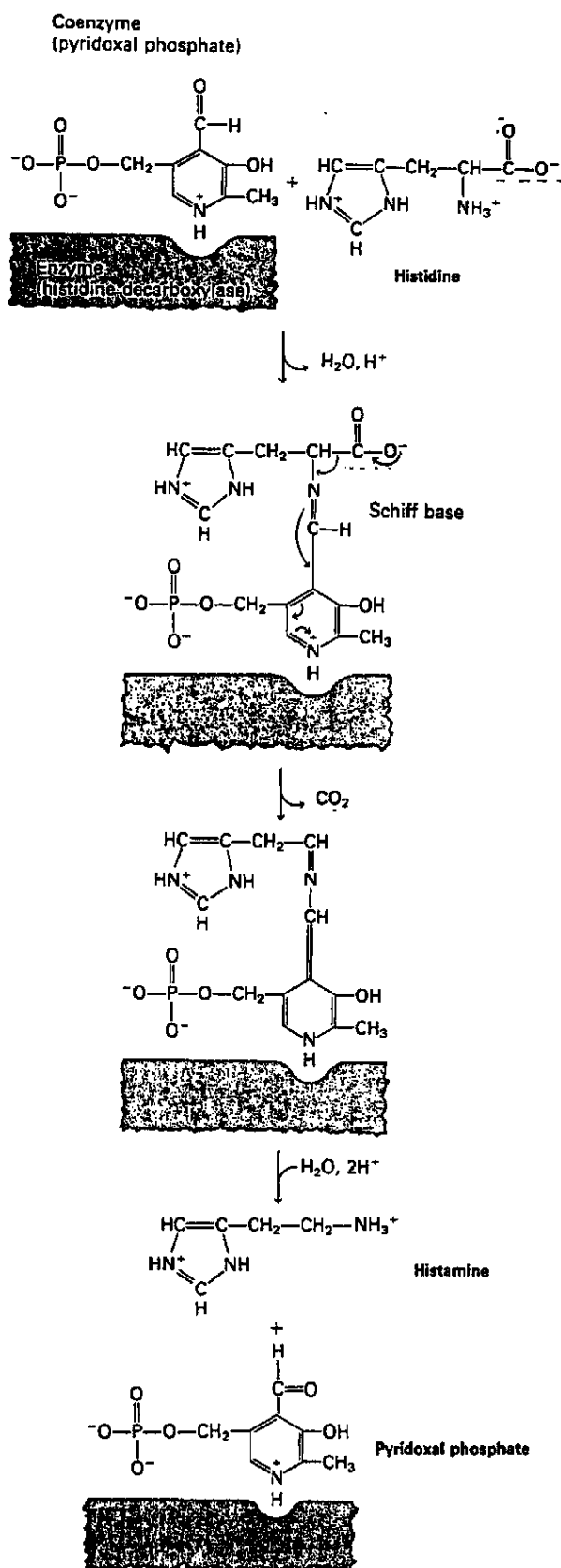
Diisopropylfluorophosphate is a potent, irreversible inhibitor of acetylcholinesterase as well as of chymotrypsin. The compound is lethal to animals because it blocks nerve transmission by causing a buildup of the transmitter substance. (The action of this transmitter is discussed in Chapter 20.)

#### Coenzymes Are Essential for Certain Enzymatically Catalyzed Reactions

Many enzymes contain a *coenzyme*—a tightly bound small molecule or prosthetic group essential to enzymatic activity. Vitamins required in trace amounts in the diet are often converted to coenzymes. Coenzyme A, for instance, is derived from the vitamin pantothenic acid; the coenzyme pyridoxal phosphate is derived from vitamin B<sub>6</sub>. To cite just one example of how coenzymes function, we consider pyridoxal phosphate. The aldehyde group



can form a covalent complex called a *Schiff base* with an  $-\text{NH}_2$  group of an amino acid, which facilitates or lowers the activation energy for the breaking of bonds to the carbon of the amino acid. Figure 2-21 shows how pyridoxal phosphate catalyzes the decarboxylation of histidine to form histamine—a potent dilator of small blood vessels. Histamine is released by certain cells in the course of allergic hypersensitivity.



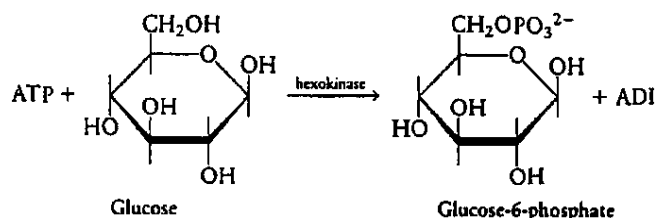
◀ **Figure 2-21** Pyridoxal phosphate, a coenzyme, participates in many reactions involving amino acids. When it is bound to histidine decarboxylase, as in this example, it forms a Schiff base with the  $\alpha$  amino group of histidine. The positive charge on the nitrogen of pyridoxal phosphate then attracts the electrons from the carboxylate group of the histidine, via a charge relay system. This weakens the bond between the  $\alpha$  carbon of the histidine and the carboxylate group, causing the release of  $\text{CO}_2$ . Finally, histamine, the reaction product, is hydrolyzed from the pyridoxal complex.

### Substrate Binding May Induce a Conformational Change in the Enzyme

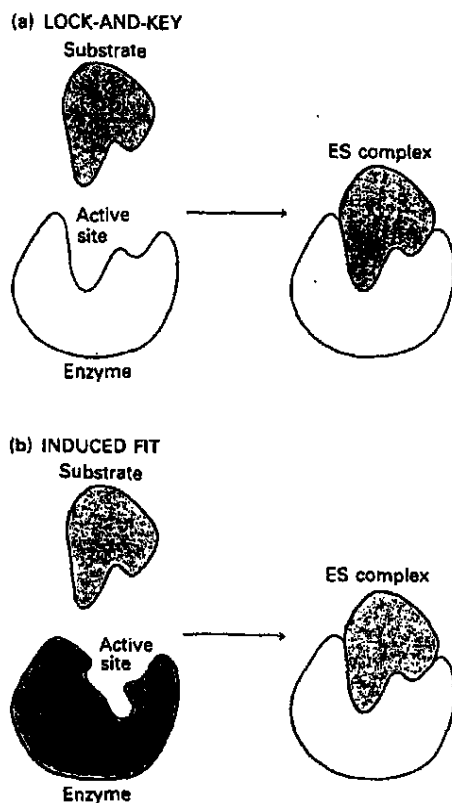
When a substrate binds to an enzyme, molecules of complementary charge or shape, or both, may simply fit together into a complex stabilized by a variety of noncovalent bonds. Such an interaction resembles the fitting of a key into a lock and is said to occur by a *lock-and-key* mechanism (Figure 2-22a).

In some enzymes, the binding of the substrate induces a conformational change in the enzyme that causes the catalytic residues to become positioned correctly. Molecules that attach to the substrate-binding site, or *recognition site*, of the enzyme but that do not induce a conformational change are not substrates of that enzyme. Thus an enzyme differentiates between a substrate and a nonsubstrate in two ways: Does the potential substrate bind to the enzyme? If so, does it induce the correct conformational change? When both criteria are met, the enzyme-substrate complex is said to demonstrate *induced fit* (Figure 2-22b).

An important example of induced fit is provided by the enzyme hexokinase, which catalyzes the transfer of a phosphate residue from ATP to a specific carbon atom of glucose:



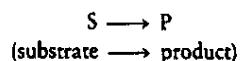
This is the first step in the degradation of glucose by cells. X-ray crystallography has shown that hexokinase consists of two domains. The binding of glucose induces a major conformational change that brings these domains closer together and creates a functional catalytic site (Figure 2-23). Only glucose and closely related molecules can induce this conformational change, ensuring that the enzyme is used to phosphorylate only the correct substrates. Molecules such as glycerol, ribose, and even water may bind to the enzyme at the recognition site but cannot induce the requisite conformational change, so they are not substrates for the enzyme.



▲ **Figure 2-22** Two mechanisms for the interaction of an enzyme and a substrate. (a) In the lock-and-key mechanism, the substrate fits directly into the binding site of the enzyme. (b) If binding occurs by induced fit, the substrate induces a conformational change in the enzyme that appropriately positions the substrate for catalysis.

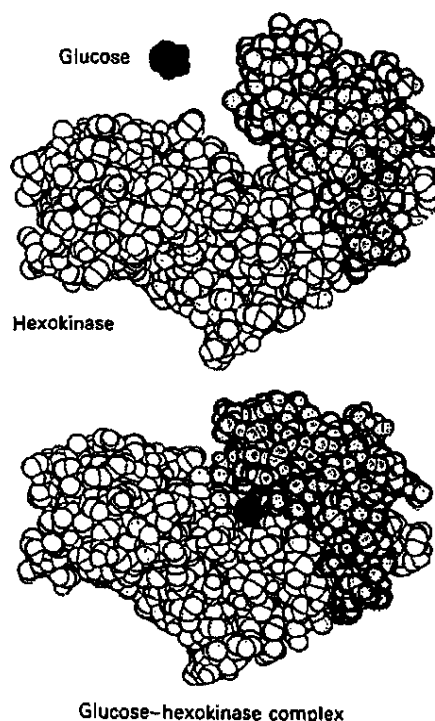
### The Catalytic Activity of an Enzyme Can Be Characterized by a Few Numbers

Enzymatic specificity is usually quantified by discrimination ratios: a good substrate may be cleaved 10,000 times as fast as a poor substrate. The catalytic power of an enzyme on a given substrate involves two numbers:  $K_m$ , which measures the affinity of the enzyme for its substrate, and  $V_{max}$ , which measures the maximal velocity of enzymatic catalysis. Equations for  $K_m$  and  $V_{max}$  are most easily derived by considering the simple reaction



in which the rate of product formation depends on  $[S]$ , the concentration of the substrate, and on  $[E]$ , the concentration of the catalytic enzyme. For an enzyme with a single catalytic site, Figure 2-24(a) shows how  $d[P]/dt$ , the rate of product production, depends on  $[S]$  when  $[E]$  is kept constant.

At low concentrations of  $S$ , the reaction rate is propor-



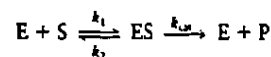
▲ **Figure 2-23** The conformation of hexokinase changes markedly when it binds the substrate glucose: the two domains of the enzyme come closer together to surround the substrate. Molecules such as the five-carbon sugar ribose can also bind to hexokinase by forming specific hydrogen bonds with groups in the substrate-binding pocket of the enzyme, but only glucose can form all of the bonds that cause the enzyme to change its conformation. *Courtesy of Dr. Thomas A. Steitz.*

tional to  $[S]$ ; as  $[S]$  is increased the rate does not increase indefinitely in proportion to  $[S]$  but eventually reaches  $V_{max}$ , at which it becomes independent of  $[S]$ .  $V_{max}$  is proportional to  $[E]$  and to a catalytic constant  $k_{cat}$  that is an intrinsic property of the individual enzyme; halving  $[E]$  reduces the rate at all values of  $[S]$  by one-half.

When interpreting curves such as those in Figure 2-24, bear in mind that all enzymatically catalyzed reactions include at least three steps: (1) the binding of the substrate ( $S$ ) to the enzyme ( $E$ ) to form an enzyme-substrate complex ( $ES$ ); (2) the conversion of  $ES$  to the enzyme-product complex ( $EP$ ); and (3) the release of the product ( $P$ ) from  $EP$ , to yield free  $P$ :



In the simplest case, the release of  $P$  is so rapid that we can write



## 62 CHAPTER 2 • MOLECULES IN CELLS

The reaction rate  $d[P]/dt$  is proportional to the concentration of ES and to the catalytic constant  $k_{cat}$  for the given enzyme:

$$\frac{d[P]}{dt} = k_{cat} [ES] \quad (1)$$

To calculate [ES], we assume the reaction is in a steady state, so that  $k_1 [E] [S]$ , the formation rate of [ES], is equal to the rate of its consumption, either by dissociation of uncatalyzed substrate at a rate of  $k_2 [ES]$  or by catalysis at a rate of  $k_{cat} [ES]$ :

$$k_1 [E] [S] = (k_2 + k_{cat}) [ES] \quad (2)$$

If

$$[E]_{tot} = [E] + [ES] \quad (3)$$

(where  $[E]_{tot}$  is the sum of the free and the complexed enzyme, or the total amount of enzyme), then we can combine equations (2) and (3) to obtain

$$\begin{aligned} [E]_{tot} &= [E] + [ES] = \frac{(k_2 + k_{cat})}{k_1 [S]} [ES] + [ES] \\ &= [ES] \left[ 1 + \left( \frac{k_2 + k_{cat}}{k_1} \right) \left( \frac{1}{[S]} \right) \right] \end{aligned}$$

If we define  $K_m$ , called the *Michaelis constant*, as

$$\frac{k_2 + k_{cat}}{k_1} \quad (4)$$

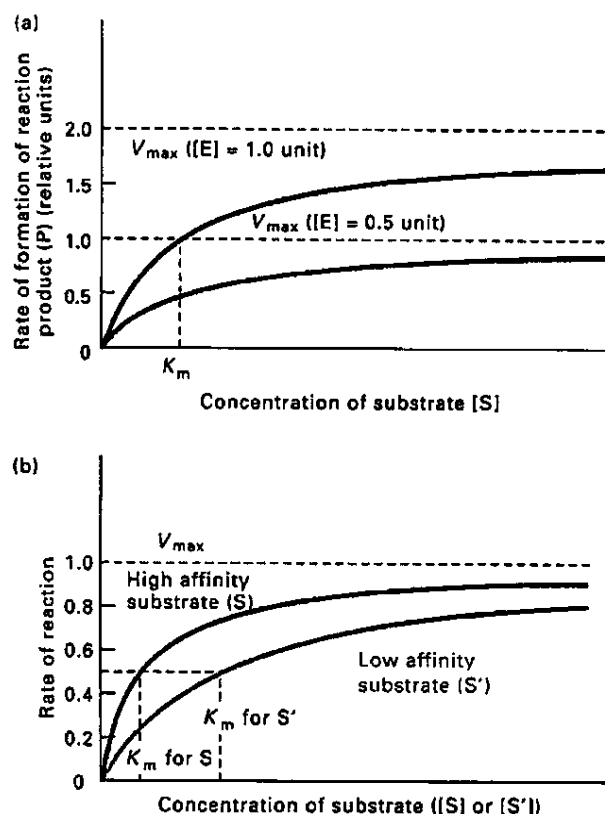
then

$$[ES] = \frac{[E]_{tot}}{1 + K_m/[S]}$$

Thus

$$\begin{aligned} \frac{d[P]}{dt} &= k_{cat} [ES] = k_{cat} [E]_{tot} \frac{1}{1 + K_m/[S]} \\ &= k_{cat} [E]_{tot} \frac{[S]}{[S] + K_m} \end{aligned} \quad (5)$$

This equation fits the curves shown in Figure 2-24a.  $V_{max}$ , which is equal to  $k_{cat} [E]_{tot}$ , is the maximal rate of product formation if all recognition sites on the enzyme are filled with substrate.  $K_m$  is equivalent to the substrate concentration at which the reaction rate is half-maximal. (If  $[S] = K_m$ , then from equation (5) we calculate the rate of product formation to be  $\frac{1}{2} k_{cat} [E]_{tot} = \frac{1}{2} V_{max}$ .) For most enzymes, the slowest step is the catalysis of [ES] to [E] + [P]. In these cases,  $k_{cat}$  is much less than  $k_2$ , so that  $K_m = (k_2 + k_{cat})/k_1 \approx k_2/k_1$  is equal to the equilibrium constant for binding S to E. Thus the parameter  $K_m$  describes the affinity of an enzyme for its substrate. The smaller the value of  $K_m$ , the more avidly the enzyme can bind the substrate from a dilute solution (Figure 2-24b) and the lower the value of [S] needed to reach half-maximal velocity. The concentrations of the various



▲ **Figure 2-24** (a) The rate of a hypothetical enzymatically catalyzed reaction  $S \rightarrow P$  for two different concentrations of enzyme [E] as a function of the concentration of substrate [S]. The substrate concentration that yields a half-maximal reaction rate is denoted by  $K_m$ . Doubling the amount of enzyme causes a proportional increase in the rate of the reaction, so that the maximal velocity  $V_{max}$  is doubled. The  $K_m$ , however, is unaltered. (b) The rates of reactions catalyzed by an enzyme with a substrate S, for which the enzyme has a high affinity, and with a substrate S', for which the enzyme has a low affinity. The  $V_{max}$  value is the same for S and S', but  $K_m$  is higher for S'.

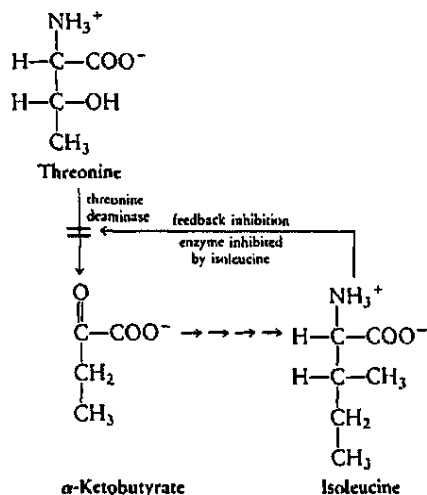
small molecules in a cell vary widely, as do the  $K_m$  values for the different enzymes that act on them. Generally, the intracellular concentration of a substrate is approximately the same as or greater than the  $K_m$  value of the enzyme to which it binds.

### The Actions of Most Enzymes Are Regulated

Many reactions in cells do not occur at a constant rate. Instead, the catalytic activity of the enzymes is *regulated* so that the amount of reaction product is just sufficient to meet the needs of the cell.

Letter Brief  
Ex. C  
D-M

**An Enzyme Can Be Feedback Inhibited in a Reaction Pathway** Consider a series of reactions leading to the synthesis of the amino acid isoleucine, which is primarily used by cells as a monomer in the synthesis of proteins. The amount of isoleucine needed depends on the rate of protein synthesis in the cell. The first step in the synthesis of isoleucine is the elimination of an amino group, which converts the amino acid threonine to the compound  $\alpha$ -ketobutyrate. Threonine deaminase—the enzyme that catalyzes this reaction—plays a key role in regulating the level of isoleucine. In addition to its substrate-binding sites for threonine, threonine deaminase contains a binding site for isoleucine. When isoleucine is bound there, the enzyme molecule undergoes a conformational change, so that it cannot function as efficiently. Thus isoleucine acts as an *inhibitor* of the reaction for the conversion of threonine. If the isoleucine concentration in the cell is high, the binding of isoleucine to the enzyme temporarily reduces the rate of isoleucine synthesis:



This is an example of *feedback inhibition*, whereby an enzyme that catalyzes one of a series of reactions is inhibited by the ultimate product of the pathway.

In isoleucine synthesis, as in most cases of feedback inhibition, the final product in the reaction pathway inhibits the enzyme that catalyzes the first step that does not also lead to other products. The suppression of enzyme function is not permanent. If the concentration of free isoleucine is lowered, bound isoleucine dissociates from the enzyme, which then reverts to its active conformation. The binding of the inhibitor isoleucine to the enzyme and its subsequent release can be described by the equilibrium-binding constant  $K_i$ , which is similar to the constant  $K_m$  used for substrate binding:

$$[E \cdot \text{Ile}]_{\text{inactive}} \xrightleftharpoons{K_i} [\text{Ile}] + [E]_{\text{active}}$$

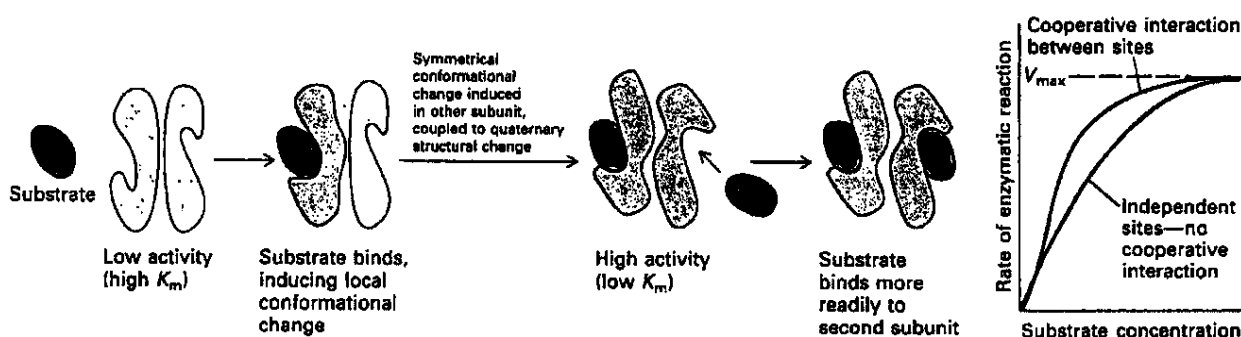
$$K_i = \frac{[\text{Ile}][E]_{\text{active}}}{[E \cdot \text{Ile}]_{\text{inactive}}}$$

**Many Enzymes Have Multiple Binding Sites for Regulatory Molecules** Some enzymes have binding sites for small molecules that affect their catalytic activity; a stimulator molecule is called an *activator*. Enzymes may even have multiple sites for recognizing more than one activator or inhibitor. In a sense, enzymes are like microcomputers; they can detect concentrations of a variety of molecules and use that information to vary their own activities. Molecules that bind to enzymes and increase or decrease their activities are called *effectors*. Effectors can modify enzymatic activity because enzymes can assume both active and inactive conformations: activators are positive effectors; inhibitors are negative effectors. Effectors bind at *regulatory sites*, or *allosteric sites* (from the Greek for “another shape”), a term used to emphasize that the regulatory site is an element of the enzyme distinct from the catalytic site and to differentiate this form of regulation from competition between substrates and inhibitors at the catalytic site.

**Multimeric Organization Permits Cooperative Interactions among Subunits** Many enzymes and some other proteins are multimeric—that is, they contain several copies, or subunits, of one or more distinct polypeptide chains. Some multimeric enzymes contain identical subunits, each of which has a catalytic site and possibly an effector site. In other enzymes, regulatory sites and catalytic sites are located on different subunits, each with a particular structure. On binding an activator, inhibitor, or substrate, a subunit undergoes a conformational change, usually small, that triggers a change in quaternary structure. This quaternary rearrangement favors a similar conformational change in the other subunits, thereby increasing their affinity for the type of ligand initially bound (Figure 2-25). When several subunits interact cooperatively, a given increase or decrease in substrate or effector concentration causes a larger change in the rate of an enzymatic reaction than would occur if the subunits acted independently. Because of such *cooperative interactions*, a small change in the concentration of an effector or substrate can lead to large changes in catalytic activity.

Cooperative interactions among the four subunits in hemoglobin demonstrate clearly the advantages of multimeric organization. The binding of an  $\text{O}_2$  molecule to any one of the four chains (each hemoglobin chain binds one  $\text{O}_2$ ) induces a local conformational change in that subunit. This change can in turn induce a large change in quaternary structure. The quaternary change involves a rearrangement of the positions of the two  $\alpha$  and two  $\beta$  chains in the tetramer. The local conformational changes that accompany  $\text{O}_2$  binding can then occur more readily in the remaining subunits, increasing their affinity for oxygen. The binding of a second  $\text{O}_2$  makes the quaternary structural change even more likely. The cooperative

## 64 CHAPTER 2 • MOLECULES IN CELLS



▲ **Figure 2-25** A cooperative interaction between active sites (two identical subunits of a hypothetical enzyme). The binding of a substrate to one subunit of a multimeric enzyme induces a conformational change in the adjacent subunit,

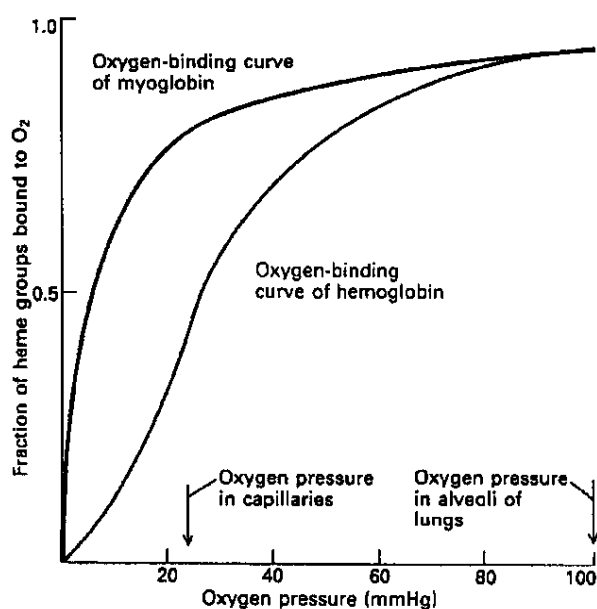
which lowers the  $K_m$  for the binding of the substrate there. Thus a small change in the substrate concentration can cause a much larger increase in the reaction rate than would occur if there were no cooperative interactions between active sites.

interaction between the chains causes the molecule to take up or lose four  $O_2$  molecules over a much narrower range of oxygen pressures than it would otherwise. As a result, hemoglobin is almost completely oxygenated at the oxygen pressure in the lungs and largely deoxygenated at the oxygen pressure in the tissue capillaries (Figure 2-26).

The contrast between hemoglobin and myoglobin is revealing. Myoglobin is a single-chain oxygen-binding protein found in muscle. The oxygen-binding curve of myoglobin has the characteristics of a simple equilibrium reaction:



Myoglobin has a greater binding affinity for  $O_2$  (a lower  $K_{O_2}$ ) than hemoglobin at all oxygen pressures. Thus, at



the oxygen pressure in capillaries,  $O_2$  moves from hemoglobin into the muscle cells, where it binds to myoglobin, ensuring the efficient transfer of  $O_2$  from blood to tissues.

The quaternary-structure rearrangements associated with multimeric organization also provide a way for the effects of activator or inhibitor binding at an allosteric site to be transmitted to a distant catalytic site without large changes in the secondary or tertiary structure of an enzyme, which would be incompatible with the principle that a particular primary structure must adopt a unique folded conformation. Thus, for example, small conformational changes in a domain in response to binding of an effector molecule would produce a quaternary-structure change, which amplifies the conformational signal and allows it to be transmitted robustly to other parts of the enzyme, where it would induce a small conformational change affecting enzymatic activity. Membrane-embedded receptor proteins that must transmit a conformational signal from one side of a membrane to the other are also likely to be multimeric; they transmit the signal by quaternary-structure rearrangement or by an effector-induced shift in the monomer-multimer equilibrium.

◀ **Figure 2-26** The binding of oxygen to hemoglobin depends on cooperative interactions between the four chains. The graph shows the fraction of heme groups in hemoglobin and in myoglobin bound to  $O_2$  as a function of the oxygen pressure. Note that the binding activity of hemoglobin increases sharply over a narrow range of oxygen pressures (20–40 mmHg). Hemoglobin is saturated with  $O_2$  in the lungs, but it releases much of its bound  $O_2$  at the low oxygen pressure in the tissue capillaries. At any oxygen pressure, myoglobin has a higher affinity for  $O_2$  than hemoglobin does. As myoglobin is a principal muscle protein, this property allows oxygen to be transferred from blood to muscle.

Letter Brief  
Ex. C  
D-M

**Enzymes Are Regulated in Many Ways** The activities of enzymes are extensively regulated so that the numerous enzymes in a cell work together harmoniously. All metabolic pathways are closely controlled at all times. Synthetic reactions occur when the products of these reactions are needed; degradative reactions occur when molecules must be broken down. Kinetic controls affecting the activities of key enzymes determine which pathways are going to be used and the rates at which they will function.

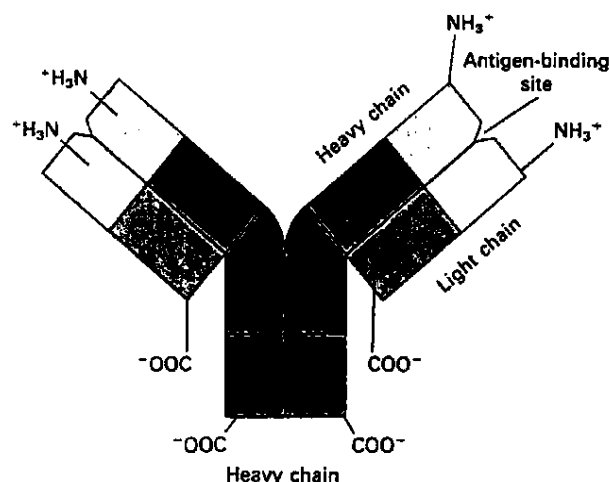
Regulation of cellular processes involves more than simply turning enzymes on and off, however. Some regulation is accomplished through *compartmentation*. Many enzymes are localized in specific compartments of the cell, such as the mitochondria or lysosomes, thereby restricting the substrates, effectors, and other enzymes with which an enzyme can interact. In addition, compartmentation permits reactions that might otherwise compete with one another in the same solution to occur simultaneously in different parts of a cell. Cellular processes are also regulated through the control of the rates of enzyme synthesis and destruction.

## Antibodies

Enzymes are not the only proteins that bind tightly and specifically to smaller compounds. The insulin receptor on the surface of a liver cell, for example, can bind to insulin so tightly that the receptors on a cell are half-saturated when the insulin concentration is only  $10^{-9}$  M. This protein does not bind to most other compounds present in blood; it mediates the specific actions of insulin on liver cells. A molecule other than an enzyme substrate that can bind specifically to a macromolecule is often called a *ligand* of that macromolecule.

The capacity of proteins to distinguish among different molecules is developed even more highly in blood proteins called *antibodies*, or *immunoglobulins*, than in enzymes. Animals produce antibodies in response to the invasion of an infectious agent, such as a bacterium or a virus. Antibodies will be discussed at length in Chapter 25. We introduce them here because they will appear as critical reagents in the discussions of many intervening chapters.

The recognition site of an antibody can bind tightly to very specific sites—generally on proteins or carbohydrates—on the surface of the infectious agent. Experimentally, animals produce antibodies in response to the injection of almost any foreign polymer; such antibodies bind specifically and tightly to the invading substance but, like enzymes, do not bind to dissimilar molecules. The antibody acts as a signal for the elimination of infectious agents. When it binds to a bacterium, virus, or virus-infected cell, certain white blood cells (leucocytes) recognize the invading body as foreign and respond by



**▲ Figure 2-27** The structure of an antibody molecule illustrated in an immunoglobulin (IgG) made of four polypeptide chains: two identical heavy chains (blue) and two identical light chains (orange). Each antigen-binding site is formed by the N-terminal segments of a heavy and a light chain. The N-termini are highly variable in sequence, giving rise to the wide range of antibody specificity.

destroying it. The specificity of antibodies is exquisite: they can distinguish between proteins that differ by only a single amino acid and between the cells of different individual members of the same species.

All vertebrates can produce a large variety of antibodies, including ones that bind to chemically synthesized molecules. Exposure to an antibody-producing agent, called an *antigen*, causes an organism to make a large quantity of different antibody proteins, each of which may bind to a slightly different region of the antigen. For a given antigen, these constellations of antibodies may differ from one member of a species to another.

Antibodies are formed from two types of polypeptides: heavy chains, each of which is folded into four domains, and light chains, each of which is folded into two domains (Figure 2-27). The N-terminal domains of both heavy and light chains are highly variable in sequence, giving rise to the specific binding characteristics of antibodies.

### Antibodies Can Distinguish among Closely Similar Molecules

The sequence of bovine insulin is identical to that of human insulin, except at three amino acids. Yet when bovine insulin is injected into people, some individuals respond by synthesizing antibodies that specifically recognize the specific amino acids in the bovine molecule, even though human beings generally do not produce anti-

# MICROBIOLOGY

## An Introduction

Gerard J. Tortora

Bergen Community College

Berdell R. Funke

North Dakota State University

Christine L. Case

Skyline College



The Benjamin/Cummings Publishing Company, Inc.

Menlo Park • California • Reading, Massachusetts

London • Amsterdam • Don Mills, Ontario • Sydney

*Sponsoring Editor:* James W. Behnke  
*Developmental Editor:* Jane R. Gillen  
*Production Editor:* Patricia S. Burner  
*Copy Editor:* Janet Greenblatt  
*Book and Cover Designer:* Michael A. Rogondino  
*Artist:* Barbara Haynes  
*Illustrator:* Michael Fornalski  
*Photo Researcher:* Carl W. May

*About the cover:* A technician is isolating plasmids, which are tiny circles of DNA found in bacteria. The plasmids are dissolved in a dye solution that fluoresces pink under ultraviolet light. Genetic engineering using plasmids is revolutionizing the biological sciences and industry (see pages 226–229 and 704–707).

Figure acknowledgments begin on page 749.

Copyright © 1982 by The Benjamin/Cummings Publishing Company, Inc.

All rights reserved. No part of this publication may be reproduced, stored in a retrieval system, or transmitted, in any form or by any means, electronic, mechanical, photocopying, recording, or otherwise, without the prior written permission of the publisher. Printed in the United States of America. Published simultaneously in Canada.

**Library of Congress Cataloging in Publication Data**

Tortora, Gerard J.

Microbiology: an introduction.

Bibliography: p.

Includes index.

1. Microbiology. I. Funke, Berdell R.

II. Case, Christine L., 1948–

III. Title.

QR41.2.T67 576 81-21712

ISBN 0-8053-9310-2 AACR2

abcdefghij-DO-898765432

The Benjamin/Cummings Publishing Company, Inc.  
2727 Sand Hill Road  
Menlo Park, California 94025

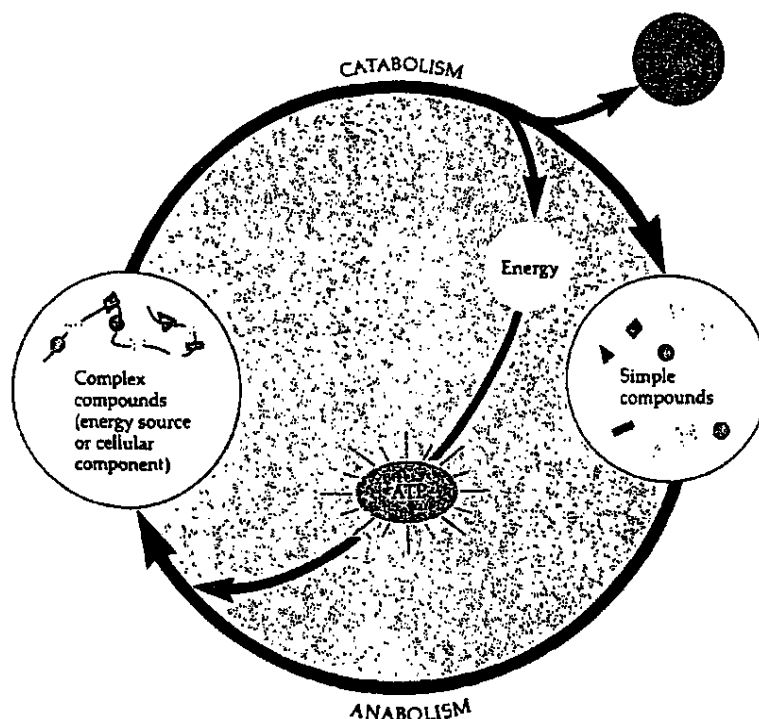
tial energy and therefore serve as energy carriers to drive energy-requiring reactions. The most common energy carrier in all biological systems is adenosine triphosphate (ATP); its structure can be reviewed in Figure 2-20. The role of ATP in the relationship between catabolic and anabolic processes is shown in Figure 5-1.

A little later in the chapter, we will examine some representative chemical reactions that deal with energy production (catabolic reactions) and energy utilization (anabolic reactions) in microorganisms. We will then look at how these various reactions are integrated within the cell. But first let us consider the principal properties of a group of proteins involved in almost all biologically important chemical reactions. These proteins, the enzymes, were described briefly in Chapter 2.

Although it is beyond the scope of this text to name and discuss the actions of individual enzymes, you should be aware of the central role of enzymes in metabolic reactions. It is important to understand that a cell's metabolic pathways are determined by its enzymes, which are, in turn, determined by its genetic makeup.

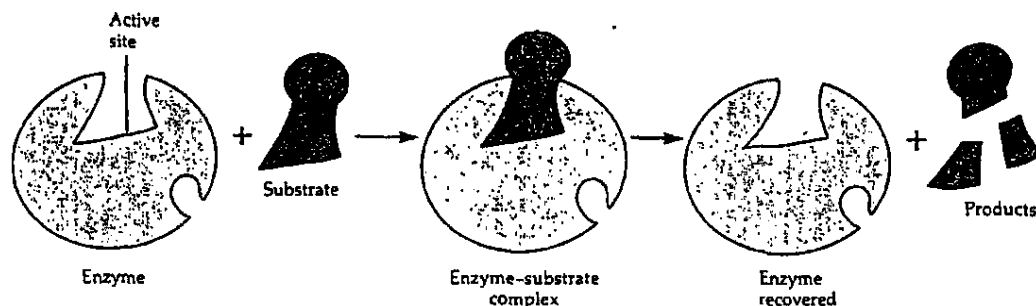
## ENZYMES

Many organic chemicals are so stable that they could remain unchanged in a cell for years. To activate these chemicals, living cells produce **enzymes**, proteins that act as catalysts in chemical reactions of importance to the cell. A *catalyst* is a substance that speeds up a reaction without being



**Figure 5-1** Relationship between anabolism and catabolism and the role of ATP. When simple compounds are combined to form complex compounds (anabolism), ATP provides the energy for synthesis. When large compounds are split apart (catabolism), heat energy is given off and some energy is trapped in ATP molecules.

## 112 Chapter 5: Microbial Metabolism



**Figure 5-2** Mechanism of enzyme action. The surface of the substrate comes into contact with the active site on the surface of the enzyme to form an enzyme-substrate complex. The substrate is then transformed into products and the enzyme is recovered.

changed by it. Generally large globular proteins, enzymes range in molecular weight from about 10,000 to somewhere in the millions. Of the thousand or more known enzymes, each has a three-dimensional characteristic shape with a specific surface configuration due to its primary, secondary, and tertiary structures (see Figure 2-18).

### Mechanism of Enzyme Action

As mentioned in Chapter 2, catalysts lower the *activation energy* required for a chemical reaction. Although scientists do not completely understand how an enzyme does this, the sequence of events is believed to be as follows (Figure 5-2):

1. The surface of the *substrate*—that is, the molecule or molecules that are reactants in the chemical reaction to be catalyzed—contacts a specific region on the surface of the enzyme molecule, called the *active site*.
2. A temporary intermediate compound called an *enzyme-substrate complex* forms.
3. The substrate molecule is transformed (by rearrangement of existing atoms, a breakdown of the substrate molecule, or the combining of several substrate molecules).
4. The transformed substrate molecules, the products of the reaction, move away from the surface of the enzyme molecule.

5. The recovered enzyme, now freed, reacts with other substrate molecules.

Enzyme reaction is characterized by its extreme *specificity* for a particular substrate. For example, a specific enzyme may be capable of hydrolyzing a peptide bond only between two specific amino acids. And other enzymes are capable of hydrolyzing starch, but not cellulose; even though both starch and cellulose are polysaccharides composed of glucose subunits, the orientations of the subunits in the two polysaccharides differ. Enzyme specificity results from the three-dimensional shape of the active site, which fits the substrate somewhat like a lock with its key. In most instances, the substrate is much smaller than the enzyme, and relatively few of the enzyme's amino acids make up the active site.

A given compound can be a substrate for a number of different enzymes that catalyze different reactions. The fate of a given reactant (substrate) depends on the specific enzyme that reacts upon it. For example, glucose-6-phosphate, an important molecule in cell metabolism, may be acted upon by at least four different enzymes, each of which will give a different product.

Enzymes are exceedingly efficient. Under optimum conditions, they can catalyze reactions at rates that are  $10^8$  to  $10^{10}$  times (up to 10 billion times) more rapid than those of comparable reactions without enzymes. The *turnover number* (number of substrate molecules metabolized per enzyme mol-

Volume I

*Todd • Sanford • Davidsohn*

CLINICAL  
DIAGNOSIS *and*  
MANAGEMENT  
by  
LABORATORY  
METHODS

*Sixteenth Edition*

JOHN BERNARD HENRY, M.D.

*Dean and Professor of Pathology, Georgetown  
University School of Medicine; Attending Pathologist,  
University Hospital, Georgetown University, Washington,  
D.C.; Formerly Professor of Pathology, College of  
Medicine, and Director of Clinical Pathology, University  
Hospital, State University of New York, Upstate  
Medical Center, Syracuse*

W. B. SAUNDERS COMPANY  
Philadelphia London Toronto

Letter Brief

Ex. C  
D-M

W. B. Saunders Company: West Washington Square  
Philadelphia, PA 19105

1 St. Anne's Road  
Eastbourne, East Sussex BN 21 3UN, England

1 Goldthorne Avenue  
Toronto, Ontario M8Z 5T9, Canada

**Library of Congress Cataloging in Publication Data**

Todd, James Campbell

Clinical diagnosis by laboratory methods.

At head of title: Todd-Sanford-Davidsohn.

Includes bibliographies.

I. Diagnosis, Laboratory. I. Sanford, Arthur Hawley, 1882-  
II. Davidsohn, Israel, 1895- III. Henry, John Bernard,  
1928- IV. Title. [DNLM: I. Diagnosis, Laboratory.  
QY4.3 T633]

RB37.T63 1979 616.07'56 77-92666

ISBN 0-7216-4639-5

Clinical Diagnosis and Management by Laboratory Methods

Volume 1 0-7216-4652-2

Volume 2 0-7216-4853-0

Single Volume 0-7216-4654-9

Set ISBN 0-7216-4639-5

© 1979 by W. B. Saunders Company. Copyright 1908, 1912, 1914, 1918, 1923, 1927, 1931, 1935, 1939, 1943, 1948, 1953, 1962, 1969 and 1974 by W. B. Saunders Company. Copyright under the International Copyright Union. All rights reserved. This book is protected by copyright. No part of it may be reproduced, stored in a retrieval system, or transmitted in any form or by any means, electronic, mechanical, photocopying, recording, or otherwise, without the written permission of the publisher. Made in the United States of America. Press of W. B. Saunders Company. Library of Congress catalog card number 77-92666.

Last digit is the print number: 9 8 7 6 5 4

Letter Brief

destruction of the red cells with higher concentrations of the abnormal hemoglobin or selective removal of the abnormal hemoglobin from the cell.

In *heterozygous alpha hemoglobinopathies*, the abnormality in the alpha chain will affect all three hemoglobin types. Therefore, six different hemoglobin types are found—the three normal hemoglobins and the three abnormal forms. Examples are Hb D<sub>Baltimore</sub>, Hb Ann Arbor, and Hb M<sub>Boston</sub>.

Combinations of abnormalities exist. *Double heterozygotes for two beta chain abnormalities* produce two different abnormal beta chains; therefore, there are two abnormal hemoglobins and no hemoglobin A. An example of this is Hb S-C disease. Double heterozygotes for beta and delta chain abnormalities and for alpha and beta chain abnormalities are rare but have provided important information. The latter will have four major hemoglobin types on electrophoresis:  $\alpha_2^A\beta_2^A$ ;  $\alpha_2^X\beta_2^A$ ;  $\alpha_2^A\beta_2^X$ ; and  $\alpha_2^X\beta_2^X$ .

*Double heterozygotes for beta hemoglobinopathy and beta thalassemia* are well known. Here, the quantity of abnormal hemoglobin exceeds the normal hemoglobin, in contrast to the heterozygous beta hemoglobinopathies, in which the reverse is true. Examples are Hb S thalassemias and Hb E thalassemia.

#### Beta hemoglobinopathies

Hemoglobins S, C, D, and E are believed to be polymorphisms because their frequency is greater than can be explained by mutation alone (Lehmann, 1977). They occur in homozygous as well as heterozygous form and involve the beta chain.

**Sickle Cell Disease.** Homozygous Hb S disease is a serious chronic hemolytic anemia, first manifest in early childhood and often fatal before the age of 30 years. With modern medical care, however, many patients live longer. Hemoglobin S is found almost exclusively in the black population; 0.1 to 0.2 per cent of the blacks born in the United States have sickle cell anemia (Schneider, 1976).

In hemoglobin S the glutamic acid in the sixth position on the beta chain is replaced by valine. This substitution is on the surface of the molecule and changes its charge and, hence, its electrophoretic mobility. Hemoglobin S is freely soluble when fully oxygenated; when oxygen is removed from Hb S, polymerization of the abnormal hemoglobin occurs, forming tactoids (fluid crystals) which are

rigid and deform the cell into the shape which gave the cell its name (Fig. 29-7). In homozygous Hb S disease, sickling occurs at physiologic oxygen tensions and the rigidity of the red cells is responsible for the hemolysis as well as for most of the complications. The rigid cells are more vulnerable to trauma and are readily trapped by the reticuloendothelial system, especially the spleen, accounting for the hemolysis. As a result of the hemolysis, severe continued marrow hyperplasia during childhood produces bone changes: expansion of the marrow space, thinning of the cortex, and radial striations seen in the skull on x-ray. Leg ulcers are common.

**COMPLICATIONS.** In early childhood, bilateral painful swelling of the dorsa of the hands or feet occurs as a result of sickling and capillary stasis; this is known as the *hand-foot syndrome* or sickle cell dactylitis. It lasts about two weeks, is accompanied by changes of periostitis as observed by x-ray, and does not occur after the age of four.

The spleen is central to three complications: A *sequestration crisis* refers to sudden pooling of blood and rapid enlargement of the spleen, resulting in hypovolemic shock. This may occur in early childhood when splenomegaly is present. *Functional asplenia* (Pearson, 1969) consists of inadequate antibody responses under some conditions and an impaired ability of the reticuloendothelial system to clear bacteria and particulate material from the blood, probably due to reticuloendothelial blockade. This may partly explain the increased risk of infection in children with the disease. Salmonella and pneumococcal infections are unusually prevalent in children with sickle cell anemia. *Autosplenectomy* is the result of vaso-occlusive episodes, resulting in progressive infarction, fibrosis, and contraction of the spleen. Though splenomegaly is present in childhood, a small fibrotic remnant is the rule in the adult.

From early childhood, patients cannot produce a concentrated urine, apparently as a result of anoxic damage to the vasa recta in the medullae of the kidneys. Hematuria as a result of papillary necrosis is common.

*Vaso-occlusive crises* are debilitating episodes of abdominal and bone or joint pain, accompanied by fever, which are probably due to plugging of small blood vessels by masses of sickled cells. Bone necrosis occurs and may be a focus for salmonella osteomyelitis. Aseptic necrosis of the femoral head is occasionally a complication. The various complications as a

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL

**EXHIBIT D**

The opinion in support of the decision being entered today is not  
binding precedent of the Board

Paper 134  
Filed: 27 July 2007

Mail Stop Interference  
P.O. Box 1450  
Alexandria, VA 22313-1450  
Tel: 571-272-4683  
Fax: 571-273-0042

UNITED STATES PATENT AND TRADEMARK OFFICE

---

BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES  
(Administrative Patent Judge Richard E. Schafer)

---

**Human Genome Sciences, Inc.,**  
Junior Party  
(Application 10/005,842-IFW  
Inventors: Jian Ni, Reiner L. Gentz,  
Guo-Liang Yu and Craig A. Rosen),

v.

**Immunex Corp.,**  
Senior Party  
(Patent 6,642,358  
Inventors: Charles Rauch and Henning Walczak).



---

Patent Interference No. 105,381 (RES)

---

Before McKELVEY, *Senior Administrative Patent Judge*, and SCHAFER  
and MOORE, *Administrative Patent Judges*.

SCHAFER, *Administrative Patent Judge*.

**Decision - Order to Show Cause**

Letter Brief  
Ex. D  
D-O

1 In a paper entered June 1, 2007, Human Genome Sciences (HGS) was  
2 put under an order to show cause why this interference should be allowed to  
3 continue and judgment should not be entered against it. HGS filed a  
4 response. HGS failed to provide sufficient reason to continue this  
5 interference and a judgment shall issue against it in a separate paper.

6 **Background**

7 This interference was declared between HGS application 10/005,842  
8 and Patent 6,642,358 assigned to Immunex Corp. Immunex was designated  
9 the senior party base upon an earlier accorded filing date of an Immunex  
10 parent application.

11 The parties filed authorized motions. HGS filed, inter alia, a motion  
12 seeking the benefit of the filing dates of certain earlier HGS applications.  
13 HGS also filed a motion asserting Immunex's involved claims were  
14 unpatentable over prior art. Immunex authorized motions included a motion  
15 asserting HGS' involved claims were unpatentable under 35 U.S.C.  
16 §§ 102(a), 102(e) and/or 103(a). HGS did not request authorization to file a  
17 responsive motion to amend any of its involved application claims. 37 CFR  
18 § 41.121(a)(2). Oppositions and replies were filed along with supporting  
19 evidence. Witnesses were cross-examined. The parties appeared before a  
20 panel of this Board and presented oral arguments on their motions.

21 In a decision on motions the panel held, inter alia, that HGS was  
22 entitled to the benefit of the filing date of one of its earlier applications, but  
23 not to the dates of the remainder. Paper 101, pp. 7-28. Accordingly the  
24 earlier filing date, however, did not change HGS' status as the junior party.  
25 HGS' motion that Immunex's claims were unpatentable was denied. Paper  
26 101, pp. 57-64.

1 The decision also granted Immunex's unpatentability motion to the  
2 extent HGS' involved claims were unpatentable under 35 U.S.C. § 102(e).  
3 HGS requested reconsideration of that decision, urging that the decision on  
4 patentability should have been deferred to the priority phase of the  
5 interference. Paper 104. The request was denied. Paper 113.

6 Since HGS was a junior party applicant with all its claims  
7 corresponding to the count held to be unpatentable, HGS was put under an  
8 order to show cause why this interference should be allowed to continue and  
9 judgment should not be entered against it. Paper 114.

### 10 **Opinion**

11 An interference is a proceeding to assist the Director in making a  
12 determination whether an involved application should issue as a patent. *See*  
13 *Karim v. Jobson*, Interference 105,376, Paper 99, p. 7 (BPAI, February 28,  
14 2007), <http://www.uspto.gov/web/offices/dcom/bpai/its/105376-99.pdf>.<sup>1</sup>

15 With respect to HGS' application, that determination has been answered in  
16 the negative because all HGS' involved claims were unpatentable over prior  
17 art. The question then arises whether this interference should continue for  
18 the sole purpose of allowing a junior party with unpatentable claims to  
19 attempt to take away senior party Immunex's patent.

20 HGS makes two principal arguments: (1) that the board is statutorily  
21 obligated to decide priority of invention and (2) that HGS will prevail on  
22 priority.

---

<sup>1</sup> The panel explained: "What the Examiner needs to know from an application v. patent interference is: Do the patent claims stand in the way of issuing a patent to the applicant? If the patentee 'loses' the interference, the patent claims are cancelled and the answer is 'No.' 35 U.S.C. § 135(a). If the applicant 'loses' the interference, then the answer is 'Yes.' A determination of unpatentability might, or might not, resolve a priority question. Once the Examiner gets a 'yes' or a 'no,' that is all the Examiner needs and that it is all the Director needs to carry out statutory duties to examine patent applications which became involved in an interference." *Karim, id.*

1 HGS first argument relies on the language in 35 U.S.C. § 135(a) that  
2 the “Board of Patent Appeals and Interferences shall determine questions of  
3 priority of the inventions and may determine questions of patentability.”  
4 According to HGS, since the question of priority remains unresolved in this  
5 interference, the statute mandates that the board conduct a priority  
6 determination. HGS relies on *Perkins v. Kwon*, 886 F.2d 325, 12 USPQ2d  
7 1308 (Fed. Cir. 1989), *Rexam Indus. Corp. v. Eastman Kodak Co.*, 182 F.3d  
8 1366, 51 USPQ2d 1457 (Fed. Cir. 1999), and *Short v. Punnonen*, 82  
9 USPQ2d 1382 (BPAI 2006).

10 None of these decisions support the proposition that the Board is  
11 compelled to determine priority under the facts here presented. In  
12 evaluating these decisions it is important to keep in mind that broad  
13 statements in judicial opinions must be interpreted in light of the issue  
14 before the court, and cannot uncritically be extended to significantly  
15 different situations. *Perez v. Department of Justice*, 480 F.3d 1309, 1312  
16 (Fed. Cir. 2007).

17 Perkins related to an interference under the 1985 interference rules  
18 (37 CFR § 1.601 *et seq* (1985)). Under the practice in effect at the time,  
19 both priority and patentability issues had been fully briefed by the parties  
20 and testimony had been submitted and cross-examined. Thus, there was a  
21 fully developed record on which to make a decision. The board decided  
22 priority of invention against Perkins, the senior party patentee. It also  
23 determined that junior party Kwon’s application claims were unpatentable  
24 under 35 U.S.C. §§ 102(b)/103. Perkins appealed to the Federal Circuit  
25 arguing that once it was determined that Kwon’s claims were unpatentable  
26 under §§ 102(b)/103, any question of priority was moot and the Board  
27 should not have considered priority. According to Perkins, the board should

1 have terminated the interference with a judgment against Kwon. The  
2 Federal Circuit affirmed the Board's decisions on patentability and priority  
3 noting that

4 decision by the Board of all issues that are fully and  
5 fairly raised during the interference proceeding, whether  
6 related to patentability or priority, is in full accord with  
7 Congressional intent that PTO procedures be simplified  
8 as well as improved . . . .

9 *Perkins*, 886 F.2d at 328, 12 USPQ2d at 1310. The court went on to state:

10 It would similarly contradict the legislative purpose if the  
11 Board were to refrain from deciding priority, when the  
12 result of such restraint would be the issuance or  
13 preservation of a facially invalid patent.

14 *Perkins*, 886 F.2d at 328, 12 USPQ2d at 1311.

15 The actual issue decided in *Perkins* was whether the board had  
16 authority to decide priority where the opponent's involved claims were held  
17 to be unpatentable. Since the board had decided priority and patentability on  
18 a fully developed record, the question that the § 135(a) compels the board to  
19 decide priority was not before the court.

20 In any event, the Federal Circuit clarified the holding of *Perkins* and  
21 other cases often cited as requiring that the Board reach a given issue in an  
22 interference, in *Berman v. Housey*, 291 F.3d 1345, 1352, 63 USPQ2d 1023,  
23 1028 (Fed. Cir. 2002). The Court stated:

24 Those cases . . . do not hold that all issues relating to  
25 patentability that are fairly raised in an interference must  
26 be addressed by the Board. Rather, those cases stand for  
27 the proposition that if, in a properly declared  
28 interference, an issue of priority or patentability is fairly  
29 raised and fully developed on the record, then the Board  
30 has the authority to consider that issue even after the  
31 Board determines that one party was not entitled to its  
32 claims.

1 *Berman*, 291 F.3d at 1352, 63 USPQ2d at 1028 (emphasis original).

2       Regarding *Perkins*, the court explained that *Perkins* held only that the  
3 Board had the authority to decide the priority issue even after it determined  
4 that Kwon's interfering claims were unpatentable. Indeed, in *Berman*, the  
5 court affirmed the board's entry of judgment without reaching priority or  
6 any other issues where the applicant's sole involved claim was barred by 35  
7 U.S.C. § 135(b). Thus, *Perkins* must be read to authorize rather than compel  
8 the Board to address priority, even if patentability is dispositive.

9       *Rexam*, like *Perkins*, involves an assertion that the priority issue  
10 should not be reached because of mootness. The interference was between  
11 Rexam's patent and Kodak's application. In the interference, Kodak proved  
12 an earlier constructive reduction to practice and the board decided priority in  
13 favor of Kodak. Rexam sought review under 35 U.S.C. § 146. During the  
14 pendency of the § 146, action a decision on priority was entered against  
15 Kodak's claims in a different interference with Avery. That decision  
16 became final. In the § 146 action, Rexam asserted that since Kodak had lost  
17 the right to the claimed subject matter in the second interference, Kodak did  
18 not have the right to contest priority in the § 146 civil action. The question  
19 was certified for an interlocutory appeal by the District Court. The Federal  
20 Circuit answered that Kodak could continue to assert priority as to Rexam  
21 notwithstanding that Kodak had lost the right to patent the subject matter.  
22 The Federal Circuit noted that

23               Priority was at issue at the Board level; it can also be at  
24 the district court level. Issues properly raised at the Board  
25 are fair ground for litigation in the district court. The  
26 public interest in ensuring that only those patents that  
27 claim patentable subject matter are issued and maintained  
28 is best served when a district court considering review of  
29 a decision of the Board resolves all issues of priority and

1 patentability that have been raised and fully developed.  
2 *Rexam*, 182 F.3d at 1370, 51 USPQ2d at 1460. Referring to *Perkins* the  
3 court stated:

4 The rationale of *Perkins* similarly applies in this case,  
5 where Kodak claims that it is entitled to defend its  
6 priority victory over *Rexam* even though it has lost  
7 priority to *Avery*. The policy behind the statute  
8 encouraging adjudication of all properly-raised issues  
9 accordingly entitles Kodak to defend its victory in the  
10 '738 interference. Public policy also favors award of the  
11 patent to the first inventor; thus, even though Kodak  
12 cannot obtain a patent for the contested subject matter  
13 because it is not the assignee of the first inventor, it  
14 should be entitled to attempt to show that *Rexam*, which  
15 similarly is not the assignee of the first inventor, is not  
16 entitled to retain its patent. The reasoning is that, if  
17 Kodak has been determined by the Board to have priority  
18 over *Rexam*, then *Avery*, which has similarly been  
19 determined to have priority over Kodak, must have  
20 priority over *Rexam*, and *Rexam* should not retain its  
21 patent.

22 *Rexam*, 182 F.3d at 1369-70, 51 USPQ2d at 1460. Thus, it was appropriate  
23 for Kodak to contest and the district court to decide priority because the  
24 issue was fairly raised and fully developed at the board. Additionally,  
25 *Rexam*'s patent was facially invalid since *Rexam*'s inventor was not the first  
26 inventor. As noted by the court: "Kodak has an interest in defending its  
27 priority judgment in order to ensure that *Rexam* does not retain an invalid  
28 patent on the interfering subject matter." *Rexam*, 182 F.3d at 1370, 51  
29 USPQ2d at 1460-61. As in *Perkins*, the issue that the Board was compelled  
30 to reach priority was not before the court since in the underlying  
31 interference, the board had decided priority.

1 HGS also relies on *Short v. Punnonen*, 82 USPQ2d 1382 (BPAI  
2 2006). *Short* is another case involving priority mootness. During that  
3 interference, Short, the junior party patentee, informed the board that he  
4 would not file a priority case. Rather, Short asserted that Punnonen's  
5 involved claim was unpatentable and the interference should be "dissolved."  
6 The board had previously denied Short's motion that Punnonen's claim was  
7 unpatentable. Short was apparently operating under the theory that a  
8 showing that senior party Punnonen's claim was unpatentable would  
9 necessarily result in a termination of the interference in junior party Short's  
10 favor. The APJ thought that Short might be confused about the status of the  
11 interference and the effect of being the junior party:

12 Short's submission shows considerable confusion about  
13 the procedural posture of the case. Rather than have  
14 Short lose immediately on the basis of this confusion, it  
15 is in the interest of justice to grant Short a very limited  
16 reprieve. Short will have a week to address its obligation  
17 to file a priority motion. If it fails to do so properly, the  
18 failure will be construed as an abandonment of contest  
19 under Bd.R. 127(b).

20 *Short*, 82 USPQ2d at 1384. The APJ went on to explain that "both the  
21 relevant rules and the case law contradict Short's proposition that a decision  
22 of unpatentability under 35 U.S.C. §§ 102 or 103 necessarily moots the  
23 priority contest." *Short*, 82 USPQ2d at 1384 (emphasis added). The APJ  
24 also quoted Perkins' statement that "[i]t would similarly contradict the  
25 legislative purpose if the Board were to refrain from deciding priority, when  
26 the result of such restraint would be the issuance or preservation of a facially  
27 invalid patent." *Short*, 82 USPQ2d at 1384. Short as the junior party had to  
28 put on a priority case in order to avoid an immediate judgment. Reminding  
29 Short of the necessity of putting on a priority case was necessary since

1 senior party Punnonen's claims were patentable and Short's patent was  
2 facially invalid. As the junior party, Short was presumptively the second  
3 inventor and the Short's claims were invalid unless priority was established.<sup>2</sup>

4 The situation here is different than the situations in *Perkins*, *Rexam*  
5 and *Short*. Unlike *Perkins* and *Rexam*, the priority case here is not fully  
6 developed. Oppositions and replies and Immunex's evidence has yet to be  
7 submitted. Additionally, Immunex is the senior party and its involved  
8 claims were not shown to be unpatentable. Indeed, HGS tried but failed to  
9 prove that Immunex's claims were unpatentable. Thus, Immunex's involved  
10 claims are not facially invalid.

11 The situation here is also different than in *Short*. Short's claims were  
12 facially invalid because Short was not the first inventor by virtue of a later  
13 filing date. Immunex's patent is not facially invalid because Immunex is the  
14 senior party and the presumptive first inventor.

15 HGS also argues that a patentability decision under § 102(e) is not a  
16 threshold issue and HGS has not waived putting on a priority case.

17 Neither argument helps HGS. The basis of the order to show cause  
18 was not that the unpatentability of HGS claims deprived HGS of standing in  
19 the interference or that HGS had waived its priority case. The basis for the  
20 order was, that the critical question of the interference has been answered  
21 and there is no longer a sufficient reason to continue the interference and put  
22 the board and the parties to the expense of presenting and evaluating  
23 priority.

24 HGS argues that there is sufficient justification to continue the  
25 interference. HGS' argument relies on distinguishing *Noelle v. Armitage*,  
26 2003 WL 21979121 (BPAI). That decision terminated an interference

---

<sup>2</sup> Short did not submit a priority case and judgment on priority was entered against Short.

1 without reaching priority when the junior party's claims were held  
2 unpatentable for failure to be supported by an enabling disclosure. HGS  
3 states that the facts here are distinguishable from those in *Noelle*. First, HGS  
4 says that the character of the enablement issue is a totally different character  
5 than unpatentability under § 102(e). HGS further says that enablement  
6 directly calls into question a party's right to continue in the interference.  
7 Unexplained, however, is why the unpatentability of a junior party  
8 applicant's claims over prior art does not equally call into question the  
9 continuance of the interference. Again, the board has answered the  
10 important question: can the director issue the patent to the applicant?

11 HGS also says a factor weighing against *Noelle* was that there was no  
12 effort made during the interference to correct the enablement problem by  
13 amending the claims or adding claims that were supported by an enabling  
14 disclosure. HGS points out that it unsuccessfully tried to amend the count.  
15 The relevance of this fact escapes us. As in *Noelle*, HGS made no attempt to  
16 correct the asserted unpatentability by seeking to file a responsive motion to  
17 amend or add claims to address the alleged unpatentability over the prior art.  
18 See 37 CFR § 41.121(a)(2).

19 Lastly, HGS argues that it has made a showing of priority far beyond  
20 that made by *Noelle*. In particular, HGS argues that it will prevail on  
21 priority and has prematurely filed its priority evidence in support of that  
22 position.

23 HGS, however, fails to explain why we should evaluate the priority  
24 case of a junior party applicant without patentable interfering claims. As  
25 noted above, Immunex's patent is senior to HGS'. Immunex's claims also  
26 withstood HGS' unpatentability challenge during the motions phase.  
27 Stopping the interference at this point before the record on priority is fully

1 developed would not leave a “facially invalid” patent. The question whether  
2 the Director can issue a patent on HGS involved application has been  
3 answered. While there is a strong public interest in resolving patent validity,  
4 resolving the validity of an issued patent is not the goal of an interference  
5 proceeding. The purpose of the interference is to resolve who between rivals  
6 of the same patentable invention should obtain the patent. It has been  
7 determined in this interference that HGS’ involved claims are unpatentable  
8 over prior art. So the determination has been made that HGS is not entitled  
9 to a patent. And senior party Immunex’s patent is not facially invalid.  
10 There is no significant need to address priority.

11 We also decline to consider HGS’s prematurely filed priority  
12 evidence. The premature submission<sup>3</sup> of HGS’ priority case does not  
13 provide an appropriate answer to the question raised by the Order to Show  
14 Cause. The Order asks why should the board evaluate priority under the

---

<sup>3</sup> HGS’ filing of its priority case was premature. The interference rules and orders established procedures by which the APJs and the board’s support staff may efficiently process interferences. An order scheduling the events in the priority phase was issued providing for Time Periods 11 to 19. The Order provides that the evidence in support of priority is not to be filed until Time Period 18. Thus, the scheduling order provided that by the end of Time Period 11:

The junior party must:

- a. File and serve a motion on priority and
- b. serve but not file evidence in support of the junior party priority case.

Paper 102, Order-Priority Times, p. 2 (emphasis original). The scheduling order also provides that the parties file supporting evidence on priority during Time Period 18:

**TIME PERIOD 18: Filing the priority record**

1. File original set of your exhibits and one copy of your exhibits;
2. For your priority motion, file one folder (three folders if an oral argument set each) containing a set of motion documents consisting of:
  - a. The priority motion,
  - b. Any corresponding opposition,
  - c. Any corresponding reply,
  - d. Any corresponding observations, and
  - e. Any corresponding response to the observations.
3. File any CD-ROM.

Paper 102, Order-Priority Times, p. 3. (emphasis added).

The submission of the supporting evidence at Time Period 18 minimizes storage and record keeping problems, eliminates the filing excess copies of exhibits, and facilitates entry of the exhibits into the interference record by the board’s support staff. The delayed filing of the record is patterned after the Federal Circuit’s delayed filing of the joint appendix. See Federal Circuit R. 30(a)(4).

1 facts of this case. HGS argument that it will prevail on priority begs the  
 2 question rather than answers it. We decline to evaluate HGS priority case to  
 3 determine if we should consider HGS' priority case.

4 **Decision**

5 HGS has failed to provide sufficient cause to continue this  
 6 interference. A judgment against HGS shall issue in a separate paper.

7

8

/Fred E. McKelvey/	)	
FRED E. McKELVEY	)	
Senior Administrative Patent Judge	)	
	)	
	)	
/Richard E. Schafer/	)	BOARD OF PATENT
RICHARD E. SCHAFER	)	APPEALS AND
Administrative Patent Judge	)	INTERFERENCES
	)	
	)	
/James T. Moore/	)	
JAMES T. MOORE	)	
Administrative Patent Judge	)	

cc(FAX):

Counsel for HUMAN GENOME  
SCIENCES, INC:  
Jorge A. Goldstein, Esq.  
STERNE, KESSLER, GOLDSTEIN  
& FOX PLLC  
1100 New York Avenue, N.W.  
Washington, D.C. 20005-3934  
Tel: 202-371-2600  
Fax: 202-371-2540  
Email: jgold@skgf.com

Counsel for IMMUNEX  
CORPORATION:  
Michael J. Wise, Esq.  
PERKINS COIE LLP  
1620 26th Street,  
6th Floor, South Tower  
Santa Monica, CA 90404-4013  
Tel: 310-788-3210  
Fax: 310-788-3399  
Email: mwise@perkinscoie.com

Attorney for GENENTECH  
(Interference 105,361):  
Oliver R. Ashe, Jr. Esq.  
ASHE, P.C.  
11440 Isaac Newton Square North  
Suite 210  
Reston, VA 20190  
Tel: 703-467-9001  
Fax: 703-467-9002  
Email: oashe@ashepc.com

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL

**EXHIBIT E**

The opinion in support of the decision being entered today is not  
binding precedent of the Board

Paper 133  
Filed: 27 July 2007

Mail Stop Interference  
P.O. Box 1450  
Alexandria, VA 22313-1450  
Tel: 571-272-4683  
Fax: 571-273-0042

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES

**Human Genome Sciences, Inc.,**  
Junior Party  
(Application 10/005,842-IFW  
Inventors: Jian Ni, Reiner L. Gentz,  
Guo-Liang Yu and Craig A. Rosen),

v.

**Immunex Corp.,**  
Senior Party  
(Patent 6,642,358  
Inventors: Charles Rauch and Henning Walczak).



Patent Interference No. 105,381 (RES)

Before Schafer, *Administrative Patent Judge*.

**Order - Expunging Paper - Bd.R. 7(a)**

- 1 A decision on the order to show cause and a judgment has been
- 2 concurrently entered in this interference. All outstanding issues are
- 3 therefore moot. No other papers other than those appropriate to the Decision
- 4 - Order to Show Cause (Paper 134) and Judgment (Paper) 135 may be filed.

Letter Brief  
Ex. E  
O-EP

Human Genome Sciences has prematurely filed its evidence in support of priority on June 18, 2007. That evidence was not to be filed until Time Period 18, January 11, 2008. Order Priority Times, Paper 102. The interference rules and orders established procedures by which the APIs and the board's support staff may efficiently process interferences. An order scheduling the events in the priority phase was issued providing for Time Periods 11 to 19. Paper 102. The Order provides that the evidence in support of priority is not to be filed until Time Period 18. Thus, the scheduling order provided that by the end of Time Period 11:

The junior party must:

- a. File and serve a motion on priority and
- b. serve but not file evidence in support of the junior party priority case.

Paper 102, Order-Priority Times, p. 2 (emphasis original). The scheduling order also provides that the parties file supporting evidence on priority during Time Period 18:

**TIME PERIOD 18: Filing the priority record**

1. File original set of your exhibits and one copy of your exhibits;
2. For your priority motion, file one folder (three folders if an oral argument set each) containing a set of motion documents consisting of:
  - a. The priority motion,
  - b. Any corresponding opposition,
  - c. Any corresponding reply,
  - d. Any corresponding observations, and
  - e. Any corresponding response to the observations.
3. File any CD-ROM.

Paper 102, Order-Priority Times, p. 3. (emphasis added). The submission of the supporting evidence at Time Period 18 minimizes storage and record keeping problems, eliminates the filing excess copies of exhibits, and

1 facilitates entry of the exhibits into the interference record by the board's  
2 support staff. The delayed filing of the record is patterned after the Federal  
3 Circuit's delayed filing of the joint appendix. See Federal Circuit R.  
4 30(a)(4).

5 The scheduling order set the TIME PERIOD 18 date for filing the  
6 priority record as January 11, 2008. Since HGS' filing is premature and  
7 since the interference has terminated by judgment without considering  
8 priority (Paper 135), HGS priority record will be expunged from the official  
9 PTO record. 37 CFR § 41.7(a). HGS may within one week of the date of  
10 this order arrange to pick-up its priority record by contacting the Interference  
11 Trial Division paralegal staff. After that date the documents will be thrown  
12 away.

/Richard E. Schafer/  
RICHARD E. SCHAFFER  
Administrative Patent Judge

cc(FAX):

Counsel for HUMAN GENOME  
SCIENCES, INC:  
Jorge A. Goldstein, Esq.  
STERNE, KESSLER, GOLDSTEIN  
& FOX PLLC  
1100 New York Avenue, N.W.  
Washington, D.C. 20005-3934  
Tel: 202-371-2600  
Fax: 202-371-2540  
Email: [jgold@skgf.com](mailto:jgold@skgf.com)

Counsel for IMMUNEX  
CORPORATION:  
Michael J. Wise, Esq.  
PERKINS COIE LLP  
1620 26th Street,  
6th Floor, South Tower  
Santa Monica, CA 90404-4013  
Tel: 310-788-3210  
Fax: 310-788-3399  
Email: [mwise@perkinscoie.com](mailto:mwise@perkinscoie.com)

Attorney for GENENTECH  
(Interference 105,361):  
Oliver R. Ashe, Jr. Esq.  
ASHE, P.C.  
11440 Isaac Newton Square North  
Suite 210  
Reston, VA 20190  
Tel: 703-467-9001  
Fax: 703-467-9002  
Email: [oashe@ashepc.com](mailto:oashe@ashepc.com)

Human Genome Sciences, Inc.

v.

Amgen, Inc. et al.

LETTER BRIEF REGARDING ISSUES ON APPEAL  
**EXHIBIT F**

HUMAN GENOME SCIENCES, INC.,  
Plaintiff,  
v.  
AMGEN INC., and IMMUNEX CORP.,  
Defendants.

:  
:  
:  
:  
:  
:  
:  
:

CIVIL ACTION  
NO. 07-526 (\*\*\*)

Wilmington, Delaware  
Wednesday, November 21, 2007 at 1:02 p.m.  
TELEPHONE CONFERENCE

BEFORE: HONORABLE MARY PAT THYNGE, U.S. MAGISTRATE JUDGE

APPEARANCES:

ASHBY & GEDDES, P.A.  
BY: JOHN G. DAY, ESQ.

and

KENYON & KENYON  
BY: RICHARD L. DeLUCIA, ESQ., and  
ALOYSIUS ANTONY PFEFFER, ESQ.  
(New York, New York)

Counsel for Plaintiff

YOUNG CONAWAY STARGATT & TAYLOR, LLP  
BY: MELANIE K. SHARP, ESQ.

and

Brian P. Gaffigan  
Registered Merit Reporter

Page 2

1 APPEARANCES: (Continued)

2 PERKINS COIE

3 BY: MICHAEL J. WISE, ESQ.,

4 LAUREN SLIGER, ESQ., and

5 JOSEPH HAMILTON, ESQ.

6 (Los Angeles, California)

7 Counsel for defendants

8 - oOo -

9 PROCEEDINGS

10 (REPORTER'S NOTE: The following telephone

11 conference was held in chambers, beginning at 1:02 p.m.)

12 THE COURT: Good afternoon, counsel. This is

13 Judge Thyne.

14 (The attorneys respond, "Good afternoon, Your

15 Honor.")

16 THE COURT: Can I please know who is on the line

17 on behalf of Human Genome?

18 MR. DAY: Good afternoon, Your Honor. On

19 behalf of Human Genome, you have John Day at Ashby & Geddes

20 locally, Rich DeLucia and Anthony Pfeffer at Kenyon & Kenyon

21 in New York.

22 THE COURT: I'm sorry. John, you are going to

23 have to do that all over again because I couldn't find a pen

24 that would write. So you have John?

25 MR. DAY: Rich DeLucia and Anthony Pfeffer from

Page 3

1 Kenyon & Kenyon.

2 THE COURT: Thank you.

3 And on behalf of Amgen/Immunex?

4 MS. SHARP: Your Honor, Melanie Sharp from Young

5 Conaway; and on the line with me are Michael Wise from

6 Perkins Coie and Lois Kwasigroch from Amgen, associate

7 general counsel there.

8 MR. WISE: Melanie?

9 THE COURT: I'm sorry.

10 MR. WISE: This is Michael Wise. May I amend

11 that? I have a couple people in my office I'd like to

12 identify for the record.

13 THE COURT: All right. Please do.

14 MR. WISE: One of my associates, Joseph

15 Hamilton, and my other associate, Lauren Sliger, both of

16 Perkins Coie appearing on behalf of Amgen/Immunex.

17 THE COURT: All right. Thank you. I have first

18 names I wrote down completely so I'm going to refer to all

19 of you on a first name basis.

20 The issue that has come to my attention is the

21 issue of how we're going to deal with trying to get a

22 schedule done in this case, and I believe a proposed

23 scheduling order was forwarded to me; is that correct?

24 MR. DeLUCIA: Yes.

25 (Unidentified speaker): Yes, it is.

Page 4

1 THE COURT: Counsel, you need to identify who  
2 you are when you are responding so that we have not just  
3 "unidentified attorney" on the record.

4 And what we're going to do about this to get the  
5 case off of first base. My understanding is that this is a  
6 patent case and I understand it's not an ANDA case; is that  
7 correct?

8 MR. DeLUCIA: Your Honor, that was Rich DeLucia.  
9 I apologize for not identifying myself. And I was agreeing  
10 that you're correct to say it is a patent case and it is not  
11 an ANDA case.

12 THE COURT: Okay.

13 MS. SHARP: Your Honor. Melanie Sharp. If I  
14 may on behalf of Amgen?

15 THE COURT: Yes.

16 MS. SHARP: This is an appeal from an  
17 interference.

18 THE COURT: I understand.

19 MS. SHARP: And in our last call, I had  
20 understood Your Honor to suggest to the parties that we meet  
21 and confer and try to sort out a few issues.

22 THE COURT: Yes, that is one of the issues in  
23 my mind, and I don't know whether the parties have been  
24 successful in doing that.

25 MS. SHARP: Michael Wise is going to speak to

Page 5

1 that on our behalf.

2 MR. WISE: Your Honor, the last time we left  
3 off, one of the big issues that the court was facing was a  
4 legal issue as to what the jurisdiction of the court is and  
5 what is properly on appeal.

6 THE COURT: Yes.

7 MR. WISE: And what you had instructed us to do  
8 is to try to meet and confer and to come to some kind of  
9 agreement as to what the issues were on the appeal. I think  
10 the meet and confer was helpful in that regard, and I'd like  
11 to give you a couple comments on it and then turn it over to  
12 my opposing counsel to make his comments.

13 THE COURT: All right.

14 MR. WISE: Again, this is Michael Wise speaking  
15 for Amgen.

16 THE COURT: Yes.

17 MR. WISE: One of the big issues we raised the  
18 last time is Phase II, if you will, of the interference, is  
19 whether or not the issue of priority is on appeal. Our  
20 position is it's not and, therefore, evidence of the  
21 inventors from each side, their conception date, their  
22 reduction to practice date, when they actually made the  
23 invention, diligence, corroborating evidence, inventor  
24 testimony, notebooks, things of that nature are not  
25 discoverable and the issue is not on appeal. I think we

Page 6

1 have not reached agreement on that issue but I'll let  
 2 opposing counsel address that in his comments.  
 3 I think at a minimum, you need to brief the  
 4 issue of whether or not the big picture issue of priority  
 5 with respect to actual invention dates is on appeal, and  
 6 that is an issue of law for the court to determine whether  
 7 it has jurisdiction to decide that issue, and also that  
 8 drives 50 percent of the discovery in the case. As I  
 9 mentioned before, there is two phases in interference, each  
 10 phase takes about ten months, and there is a lot of evidence  
 11 that goes in before the board renders its decision and Phase  
 12 II did not get completed in this action and we think the  
 13 issue of priority is not on appeal.

14 THE COURT: All right. I understand that.

15 MR. WISE: The second part is I think you had  
 16 mentioned you had difficulty finding recent case law on 146  
 17 actions in our last phone call.

18 THE COURT: I did, yes.

19 MR. WISE: And I managed to find the most recent  
 20 statement from the Federal Circuit that was issued in August  
 21 of this year, and it goes to one of the very issues that I  
 22 was trying to articulate in the last conference call, and  
 23 the issue is this: We may both agree that there is an  
 24 overarching legal issue that is on appeal but the devil is  
 25 in the detail and what the Federal Circuit says is you are

Page 7

1 limited to the legal theories that were presented before.  
 2 Now, let me just quote what the court says. This is the  
 3 Boston Scientific case and the Fed Circuit cite for you is  
 4 497 F.3d 1293.

5 The court says: A party may not, however,  
 6 advance new legal theories at the trial court level even if  
 7 the overarching legal issue was presented below. An action  
 8 under 35 U.S.C. 146 is essentially a proceeding to review  
 9 the action of the board. The parties to an interference  
 10 must make a complete presentation of the issues at the  
 11 board level so that the interference is efficient and not  
 12 wasteful of administrative and judicial resources. Failure  
 13 to advance legal theories before the board constitutes a  
 14 failure to make a complete presentation of the issues and  
 15 permitting a party to raise those theories for the first  
 16 time before the trial court would be both inefficient and  
 17 wasteful of administrative and judicial resources.

18 And that is the reason we want to brief what the  
 19 issues are on appeal in this case at the get-go, so we don't  
 20 waste a lot of resources.

21 THE COURT: So what did you actually agree?

22 MR. WISE: We agreed there were some overarching  
 23 legal issues that were on appeal but the devil is in the  
 24 detail, and I think we disagree as to what the legal  
 25 theories are appropriately on review and therefore what the

Page 8

1 appropriate scope of the discovery is.

2 THE COURT: Okay.

3 MR. WISE: That's the problem. For example,  
 4 there are several decisions issued by the board that we  
 5 believe are appropriately reviewed for abuse of discretion  
 6 because the board was applying its permissive rules of  
 7 procedure and they did not follow procedure right. Their  
 8 motions were denied. That is reviewed on an abuse of  
 9 discretion which, by definition, if the court is sitting  
 10 an appellate court, reviewing a lower court for abuse of  
 11 discretion, you look to the administrative record and there  
 12 is no more discovery necessary.

13 THE COURT: Let me ask you this: Did the two  
 14 of you agree that the issue needs to be briefed before the  
 15 court can figure out what its jurisdiction is supposed to  
 16 be?

17 MR. DeLUCIA: No, Your Honor. Rich DeLucia.  
 18 May I address the court?

19 THE COURT: Yes, you may.

20 MR. DeLUCIA: First of all, we're here on a Rule  
 21 26 scheduling conference and Mr. Wise and Amgen/Immunex are  
 22 raising effectively a preclusion request as to the scope  
 23 of this review. And they're using words "on appeal," et  
 24 cetera. 35 U.S.C. 146 gives the court jurisdiction. They  
 25 agree that we're seeking review of the interference, that

Page 9

1 there are clear issues that have been identified that we  
 2 agree are subject to that review. There is going to be a  
 3 trial. It is conventional for there to be fact discovery in  
 4 these actions. The case cited to you does not stand for the  
 5 jurisdiction of the court. It is not anything that goes to  
 6 a matter that precludes entry of a scheduling order.

7 On this issue of scope of review that we're  
 8 talking about, at trial, in most cases, all cases that I've  
 9 been involved in, there are motions to preclude evidence  
 10 as irrelevant and not properly considered at trial. That  
 11 is the time those issues come up for this very important  
 12 reason. And the case cited to you for the proposition it  
 13 was cited, A, I think counsel will admit does not go to the  
 14 issue of jurisdiction. It goes to a different question. So  
 15 jurisdiction is not on the table and this court's ability to  
 16 enter a scheduling order is not on the table.

17 The issue of what is admissible at trial Mr.  
 18 Wise has every right to raise at the appropriate time. The  
 19 interference is appealed by Human Genome scientists. We  
 20 appealed the interference record. It goes into evidence as  
 21 a matter of statutory right.

22 The scope of review, here is a case that  
 23 directly deals with that. It's called Conservallite v  
 24 Whitmeyer -- it's frequently, frequently cited -- 21 F.3d  
 25 198. The interference issues decided by the Patent Office

Page 10

1 are subject to review trial de novo by the District Court,  
 2 A. That is black letter law. Everybody agrees with  
 3 that. B. Even on issues that were never raised at the  
 4 interference level at all -- issues never raised, this is  
 5 the case law from the Federal Circuit -- under appropriate  
 6 circumstance, a District Court may exercise its discretion  
 7 and admit testimony on issues even though they were not  
 8 even raised before the board.  
 9 So after discovery, if Mr. Wise says Mr. DeLucia  
 10 is pursuing an irrelevant matter, the court should deny his  
 11 right to go forward at trial on something not even within  
 12 the matters decided by the board. The court has discretion  
 13 to decide the scope of the review it will do. For us to be  
 14 engaged now, prior to entry of a scheduling order, in trying  
 15 to jump forward to the point in time when the scope of the  
 16 pretrial order will define those issues is simply an effort  
 17 by counsel to preclude and complicate the discovery process.  
 18 If counsel, after I serve a document request or  
 19 interrogatory, says it's not fair game, it's never going to  
 20 be considered or the like and therefore not reasonably  
 21 calculated to lead to discoverable evidence -- which, by the  
 22 way, would be an extraordinary ruling in a case like this --  
 23 that can be raised at the appropriate time in context, tied  
 24 to relevant issues. Deciding up front and counsel saying  
 25 issues like that is not properly on appeal, we deny the

Page 11

1 court should consider that, is seeking preclusion and  
 2 building and asking this court to rule on things before  
 3 they're in issue and inviting potential error into this  
 4 record and it's before discovery has gotten started in the  
 5 discovery context. There is nothing different about this  
 6 action that would justify that sort of preclusive action  
 7 and the only remedy I'm asking for right now is to have a  
 8 schedule in place so that we can get on with discovery.  
 9 THE COURT: No, your remedy is asking for a  
 10 schedule in place that covers everything; right?  
 11 MR. DeLUCIA: Well, covers everything that  
 12 the federal rules say is reasonably calculated to lead to  
 13 admissible evidence.  
 14 THE COURT: What was the citation for the case  
 15 that you are relying upon?  
 16 MR. DeLUCIA: I can give you a couple cases,  
 17 Your Honor.  
 18 THE COURT: No, the one that you already cited.  
 19 MR. DeLUCIA: Okay. 21 F.3d 1098.  
 20 THE COURT: 109?  
 21 MR. DeLUCIA: 1098.  
 22 MR. WISE: When it's my turn, Your Honor, may I?  
 23 MR. DeLUCIA: Your Honor, if I could just give  
 24 you? I can give you a whole bunch of cases but there is one  
 25 other I would cite you to. I'll just mention Winner v Wang,

Page 12

1 202 F.3d 1340. And what would be interesting is to take a  
 2 look at Judge Newman's -- there is a lot of interesting  
 3 things in the case but Judge Newman's concurrence where she  
 4 states emphatically what I understand to be the case in this  
 5 jurisdiction as well: That during a 146 action -- actually,  
 6 it's in the case I cited earlier, it's in the Conservallite  
 7 case with Judge Newman. In a proceeding under 146, the  
 8 parties --  
 9 THE COURT: What page?  
 10 MR. DeLUCIA: I'm at page -- let me see the  
 11 actual page of the decision here. 1105 of the Conservallite  
 12 case. This is Judge Newman in her concurrence.  
 13 THE COURT: In her concurrence? Because she  
 14 concurred and also dissented in part.  
 15 MR. DeLUCIA: Yes, that's correct. But this is  
 16 actually --  
 17 THE COURT: How about --  
 18 MR. DeLUCIA: Yes. All she says there that I'm  
 19 citing this for is what cannot be reasonably disputed, which  
 20 is in a proceeding under 146, the parties can create a new  
 21 record, present new witnesses, advance new evidence, blah  
 22 blah blah, highlighting the fact that it is a trial de novo  
 23 on the issues that the court has to decide it has discretion  
 24 on and says should be renewed during the trial. So all  
 25 we're asking for is a discovery schedule, and certainly

Page 13

1 anything that is deemed irrelevant, not fairly within  
 2 the scope of discovery, as I know, Judge Thyng, you are  
 3 accustomed to ruling, we can sharpen our focus and, if there  
 4 is a dispute, do that. I suspect there won't be a lot of  
 5 disputes.  
 6 MR. WISE: Your Honor?  
 7 THE COURT: Yes.  
 8 MR. WISE: My turn?  
 9 THE COURT: Yes.  
 10 MR. WISE: First of all, we fundamentally  
 11 disagree because the issues on appeal on a 146 action are  
 12 limited to the issues that were raised below and decided by  
 13 the board. That is black letter law. This is an issue of  
 14 law as to what is on appeal.  
 15 THE COURT: You know what? This is what I'm  
 16 going to solve, counsel. Rather than me sitting here trying  
 17 to listen to this in argument, I think that you can probably  
 18 do very abbreviated briefing on this particular issue. I  
 19 know what your argument is, Rich: De novo review. De novo  
 20 review can mean a whole host of things, as I have since  
 21 learned when I looked at the different rules of procedure,  
 22 and I think that you can probably do a letter briefs on  
 23 this; correct, counsel? Probably five, seven-page letter  
 24 briefs?  
 25 MR. WISE: From each side, Your Honor?

Page 14

1 THE COURT: Yes.

2 MR. WISE: The issues are relatively complex and

3 there are three different levels of review in a 146 action.

4 THE COURT: Yes.

5 MR. DeLUCIA: I think we can accommodate that,

6 Your Honor.

7 MR. WISE: I don't understand what the court is

8 asking, Your Honor.

9 THE COURT: I'm asking, you have a 146 action

10 brought in this court. The dispute between the two sides,

11 from what I'm able to understand, is exactly how far the

12 review can go by this court; correct?

13 MR. WISE: That's correct, Your Honor.

14 THE COURT: All right. So my question to you

15 was, do you think you can do abbreviated briefing and

16 possibly do it in a letter format of seven pages each

17 explaining to me what the law is and why, for example,

18 defendants are saying it's a de novo review and it's limited

19 entirely to what happened before, the court cannot do a

20 review beyond that. This is the reason why our argument

21 is that discovery should be so limited. Or, from the

22 plaintiff's standpoint, judge, it's broader than that and

23 you have got the right to be able to go beyond that.

24 MR. WISE: My answer to you is, yes, we can do

25 that, Your Honor. This is Michael Wise.

Page 15

1 THE COURT: Now, my question to both of you is

2 have I summarized what the issue really is that prevents us

3 from getting a scheduling order in place?

4 MR. DeLUCIA: I think Your Honor has identified

5 the dispute and we can address it in our letters, and I

6 think that will help the court make the decision.

7 THE COURT: Focus. Yes, focus. And to the

8 extent you rely on any cases, just tee them up. I was going

9 through the cases that you cited now, based upon the limited

10 library that I'm sitting in right now, just to try to read

11 it. And I understand what you are arguing about with Judge

12 Newman but I would like to know what the basis is, what the

13 arguments are. Focus the arguments, show me the cases. Do

14 you think seven pages each will be enough? Do you want to

15 do simultaneous submissions? Tell me.

16 MR. DeLUCIA: This is Rich. If you ask me, I

17 think seven pages is probably too much. I would be happy to

18 stipulate to three pages each. And what I would ask counsel

19 right now to try to facilitate this is I don't think anybody

20 is arguing on the issues that we discussed during our

21 conference call.

22 MR. WISE: Well, I disagree with you.

23 MR. DeLUCIA: Okay. Well, let's, rather than

24 raising a new round of disputes -- and I accept that when

25 Michael says there is a dispute that there is a dispute --

Page 16

1 that five pages each, if the court would like us to do it

2 simultaneously, I'm happy.

3 THE COURT: I'm asking for guidance from counsel

4 whether it makes a bit of difference because what has been

5 raised to me by both of you is that this is a purely legal

6 argument. Now, if you want to do what the position of the

7 defendant is because that was whose comments were first

8 listed in the letter of November 9th and the defendant goes

9 first and then plaintiff responds, fine.

10 MR. DeLUCIA: That's the deal, Your Honor.

11 THE COURT: Okay. And I go back to my question.

12 Is one submission, seven pages each, in a letter format

13 going to be enough pages or does counsel feel they need a

14 little bit more leeway? I know that Rich has indicated to

15 me he doesn't think you need any more. I'm just trying to

16 find out.

17 MR. WISE: Your Honor, Michael Wise. I think

18 that from their perspective, they're happy with a very short

19 brief. Because we fundamentally disagree, I would like a

20 little more length because I have ten pages.

21 THE COURT: Fine, you have ten pages. You have

22 ten pages each. But, again, the issue I stated, I just want

23 to make sure that I'm understanding that I have correctly

24 stated it for both parties.

25 MR. DeLUCIA: Your Honor, I think you have. And

Page 17

1 it is Rich. And, well, if we, when looking at the

2 transcript, if we think there should be refinement, maybe

3 we'll just let you know, if that is okay.

4 THE COURT: Okay. And my feeling is this: Now,

5 I haven't heard from Michael as to whether or not he agrees

6 that the court has defined the issue appropriately, I don't

7 think.

8 MR. WISE: I think you have, Your Honor. I

9 think the issue is, if I correctly understand it, there is a

10 legal issue as to what is properly on appeal in this action

11 and that drives the jurisdiction of the court and

12 necessarily the appropriate discovery.

13 THE COURT: That's right. They go hand in hand

14 as far as I'm concerned.

15 MR. WISE: I agree.

16 THE COURT: Timing. Michael, since it's your

17 issue, in my mind, because you want to limit discovery, your

18 submission would be due -- today is what, the 21st? I

19 recognize we're approaching Thanksgiving. How about the

20 second Monday after Thanksgiving? I haven't figured out the

21 day of that, I just threw that out.

22 MR. WISE: Second Monday after Thanksgiving --

23 THE COURT: The first Monday should be --

24 MR. WISE: -- would be the 3rd of December.

25 Your Honor, could I have until the 7th, that Friday?

Page 18

1 THE COURT: The 7th would land on a Friday;  
 2 correct?  
 3 MR. WISE: That's right, Your Honor.  
 4 THE COURT: That's fine. And, Rich, how much do  
 5 you need? Two weeks?  
 6 MR. DeLUCIA: How about a week later?  
 7 THE COURT: You want your submission due then on  
 8 December 14th?  
 9 MR. DeLUCIA: Yes. I mean if I had my  
 10 druthers, Your Honor -- here is the issue I think I'm going  
 11 to confront with this. Today is the 21st and we're talking  
 12 about their briefing due the 7th, which is over two weeks  
 13 from today, for a matter I would submit to the court is  
 14 straightforward. And that would give me five days to  
 15 respond. The court would have to rule and we're getting de  
 16 facto here a stay of discovery which I vigorously maintain  
 17 is absolutely not justified. And if I had my druthers, I'd  
 18 request the court rule that they submit their brief in a  
 19 week, I submit my brief a week later, and at least that way  
 20 the ball is moving. We're foreclosing discovery in a  
 21 scheduling order in the case at this point.  
 22 THE COURT: Well, you are not foreclosing  
 23 discovery, you're not disclosing discovery, one way or the  
 24 other. I'm sure one side or the other will remind me that  
 25 you are around. The reason I gave a little bit more time is

Page 19

1 the fact that we have Thanksgiving in between.  
 2 MR. DeLUCIA: Right, Thanksgiving is tomorrow.  
 3 THE COURT: Tomorrow, and the court is closed on  
 4 Friday. So even if you did a submission on Friday, I'm not  
 5 going to be around to get it or look at it or read it.  
 6 MR. DeLUCIA: Then can I propose the 3rd and the  
 7 10th? December 3rd and December 10th?  
 8 THE COURT: Well, that's what I threw out to you  
 9 to begin with.  
 10 MR. DeLUCIA: Yes, at least that keeps it  
 11 moving.  
 12 MR. WISE: Your Honor, how about splitting the  
 13 difference, make it the 5th and 12?  
 14 THE COURT: Make it the 5th and the 12th. Just  
 15 do it, counsel. You have 10 pages. I look forward to  
 16 seeing your submissions. The only concern I have is that  
 17 if you, for some reason, have anything that is highly  
 18 confidential in it, when you do an e-filing of it, I can't  
 19 access it off of e-file.  
 20 MR. DeLUCIA: Right.  
 21 THE COURT: So I can't imagine you are going to  
 22 throw in anything highly confidential, but if you do that,  
 23 you must submit a copy to chambers or a copy in the clerk's  
 24 office that I can access within an hour of the time that the  
 25 filing is made, the e-filing is made.

Page 20

1 MS. SHARP: Understood, Your Honor.  
 2 THE COURT: Because otherwise I just can't get  
 3 to it. I can't get to the document at all. Okay?  
 4 MR. WISE: All right.  
 5 MR. DeLUCIA: Happy Thanksgiving.  
 6 THE COURT: Happy Thanksgiving to all of you.  
 7 I don't intend to necessarily do a separate  
 8 order in this case. Please use the transcript of these  
 9 proceedings to be the court's order.  
 10 MR. DeLUCIA: Thank you very much.  
 11 MS. SHARP: Thank you, Your Honor. Happy  
 12 Thanksgiving.  
 13 THE COURT: Happy Thanksgiving, and a safe one,  
 14 too. Good-bye now.  
 15 (Telephone conference ends at 1:28 p.m.)  
 16  
 17  
 18  
 19  
 20  
 21  
 22  
 23  
 24  
 25

<b>A</b>	10:2 17:5	<b>arguments</b>	12:21,22,22	<b>chambers</b>
<b>abbreviated</b>	<b>alloysius</b>	15:13,13	<b>board</b>	2:11 19:23
13:18 14:15	1:18	<b>articulate</b>	6:11 7:9,11,13 8:4	<b>circuit</b>
<b>ability</b>	<b>amend</b>	6:22	8:6 10:8,12 13:13	6:20,25 7:3 10:5
9:15	3:10	<b>ashby</b>	<b>boston</b>	<b>circumstance</b>
<b>able</b>	<b>amgen</b>	1:15 2:19	7:3	10:6
14:11,23	1:6 3:3,6,16 4:14	<b>asking</b>	<b>brian</b>	<b>citation</b>
<b>absolutely</b>	5:15 8:21	11:2,7,9 12:25	1:24	11:14
18:17	<b>anda</b>	14:8,9 16:3	<b>brief</b>	<b>cite</b>
<b>abuse</b>	4:6,11	<b>associate</b>	6:3 7:18 16:19	7:3 11:25
8:5,8,10	<b>angeles</b>	3:15	18:18,19	<b>cited</b>
<b>accept</b>	2:5	<b>associates</b>	<b>briefed</b>	9:4,12,13,24
15:24	<b>answer</b>	3:14	8:14	11:18 12:6 15:9
<b>access</b>	14:24	<b>attention</b>	<b>briefing</b>	<b>citing</b>
19:19,24	<b>anthony</b>	3:20	13:18 14:15 18:12	12:19
<b>accommodate</b>	2:20,25	<b>attorney</b>	<b>briefs</b>	<b>civil</b>
14:5	<b>antony</b>	4:3	13:22,24	1:4
<b>accustomed</b>	1:18	<b>attorneys</b>	<b>broader</b>	<b>clear</b>
13:3	<b>anybody</b>	2:14	14:22	9:1
<b>action</b>	15:19	<b>august</b>	<b>brought</b>	<b>clerks</b>
1:4 6:12 7:7,9	<b>apologize</b>	6:20	14:10	19:23
11:6,6 12:5 13:11	4:9		<b>building</b>	<b>closed</b>
14:3,9 17:10	<b>appeal</b>	<b>B</b>	11:2	19:3
<b>actions</b>	4:16 5:5,9,19,25	<b>back</b>	<b>bunch</b>	<b>coie</b>
6:17 9:4	6:5,13,24 7:19,23	16:11	11:24	2:3 3:6,16
<b>actual</b>	8:23 10:25 13:11	<b>ball</b>		<b>come</b>
6:5 12:11	13:14 17:10	18:20	<b>C</b>	3:20 5:8 9:11
<b>address</b>	<b>appealed</b>	<b>base</b>	<b>calculated</b>	<b>comments</b>
6:2 8:18 15:5	9:19,20	4:5	10:21 11:12	5:11,12 6:2 16:7
<b>administrative</b>	<b>appearances</b>	<b>based</b>	<b>california</b>	<b>complete</b>
7:12,17 8:11	1:13 2:1	15:9	2:5	7:10,14
<b>admissible</b>	<b>appearing</b>	<b>basis</b>	<b>call</b>	<b>completed</b>
9:17 11:13	3:16	3:19 15:12	4:19 6:17,22	6:12
<b>admit</b>	<b>appellate</b>	<b>beginning</b>	15:21	<b>completely</b>
9:13 10:7	8:10	2:11	<b>called</b>	3:18
<b>advance</b>	<b>applying</b>	<b>behalf</b>	9:23	<b>complex</b>
7:6,13 12:21	8:6	2:17,19 3:3,16	<b>case</b>	14:2
<b>afternoon</b>	<b>approaching</b>	4:14 5:1	3:22 4:5,6,6,10,11	<b>complicate</b>
2:12,14,18	17:19	<b>believe</b>	6:8,16 7:3,19 9:4	10:17
<b>agree</b>	<b>appropriate</b>	3:22 8:5	9:12,22 10:5,22	<b>conaway</b>
6:23 7:21 8:14,25	8:1 9:18 10:5,23	<b>beyond</b>	11:14 12:3,4,6,7	1:21 3:5
9:2 17:15	17:12	14:20,23	12:12 18:21 20:8	<b>conception</b>
<b>agreed</b>	<b>appropriately</b>	<b>big</b>	<b>cases</b>	5:21
7:22	7:25 8:5 17:6	5:3,17 6:4	9:8,8 11:16,24	<b>concern</b>
<b>agreeing</b>	<b>arguing</b>	<b>bit</b>	15:8,9,13	19:16
4:9	15:11,20	16:4,14 18:25	<b>certainly</b>	<b>concerned</b>
<b>agreement</b>	<b>argument</b>	<b>black</b>	12:25	17:14
5:9 6:1	13:17,19 14:20	10:2 13:13	<b>cetera</b>	<b>concurred</b>
<b>agrees</b>	16:6	<b>blah</b>	8:24	12:14

<b>concurrency</b> 12:3,12,13	5:13,16 6:6,14,18 7:2,5,6,16,21 8:2	<b>decisions</b> 8:4	<b>disclosing</b> 18:23	19:18,25
<b>confer</b> 4:21 5:8,10	8:9,10,10,13,15 8:18,19,24 9:5	<b>deemed</b> 13:1	<b>discoverable</b> 5:25 10:21	<b>emphatically</b> 12:4
<b>conference</b> 1:10 2:11 6:22 8:21 15:21 20:15	10:1,6,10,12 11:1 11:2,9,14,18,20 12:9,13,17,23	<b>defendant</b> 16:7,8	<b>discovery</b> 6:8 8:1,12 9:3 10:9,17 11:4,5,8 12:25 13:2 14:21 17:12,17 18:16,20 18:23,23	<b>ends</b> 20:15
<b>confidential</b> 19:18,22	13:7,9,15 14:1,4,7 14:9,10,12,14,19	<b>defendants</b> 1:7 2:6 14:18	<b>discretion</b> 8:5,9,11 10:6,12 12:23	<b>engaged</b> 10:14
<b>confront</b> 18:11	15:1,6,7 16:1,3,11 16:21 17:4,6,11	<b>define</b> 10:16	<b>discussed</b> 15:20	<b>enter</b> 9:16
<b>conservallite</b> 9:23 12:6,11	17:13,16,23 18:1 18:4,7,13,15,18 18:22 19:3,3,8,14 19:21 20:2,6,13	<b>defined</b> 17:6	<b>dispute</b> 13:4 14:10 15:5 15:25,25	<b>entirely</b> 14:19
<b>consider</b> 11:1	<b>courts</b> 9:15 20:9	<b>definition</b> 8:9	<b>disputed</b> 12:19	<b>entry</b> 9:6 10:14
<b>considered</b> 9:10 10:20	<b>covers</b> 11:10,11	<b>delaware</b> 1:2,9	<b>disputes</b> 13:5 15:24	<b>error</b> 11:3
<b>constitutes</b> 7:13	<b>create</b> 12:20	<b>delucia</b> 1:18 2:20,25 3:24 4:8,8 8:17,17,20 10:9 11:11,16,19 11:21,23 12:10,15 12:18 14:5 15:4 15:16,23 16:10,25 18:6,9 19:2,6,10 19:20 20:5,10	<b>dissented</b> 12:14	<b>esq</b> 1:15,18,18,22 2:3 2:4,4
<b>context</b> 10:23 11:5	<hr/> <b>D</b> <hr/>	<b>denied</b> 8:8	<b>district</b> 1:1,2 10:1,6	<b>essentially</b> 7:8
<b>continued</b> 2:1	<b>date</b> 5:21,22	<b>deny</b> 10:10,25	<b>document</b> 10:18 20:3	<b>et</b> 8:23
<b>conventional</b> 9:3	<b>dates</b> 6:5	<b>detail</b> 6:25 7:24	<b>doing</b> 4:24	<b>everybody</b> 10:2
<b>copy</b> 19:23,23	<b>day</b> 1:15 2:18,19,25 17:21	<b>determine</b> 6:6	<b>drives</b> 6:8 17:11	<b>evidence</b> 5:20,23 6:10 9:9 9:20 10:21 11:13 12:21
<b>corp</b> 1:6	<b>days</b> 18:14	<b>devil</b> 6:24 7:23	<b>druthers</b> 18:10,17	<b>exactly</b> 14:11
<b>correct</b> 3:23 4:7,10 12:15 13:23 14:12,13 18:2	<b>de</b> 10:1 12:22 13:19 13:19 14:18 18:15	<b>difference</b> 16:4 19:13	<b>due</b> 17:18 18:7,12	<b>example</b> 8:3 14:17
<b>correctly</b> 16:23 17:9	<b>deal</b> 3:21 16:10	<b>different</b> 9:14 11:5 13:21 14:3	<hr/> <b>E</b> <hr/>	<b>exercise</b> 10:6
<b>corroborating</b> 5:23	<b>deals</b> 9:23	<b>difficulty</b> 6:16	<b>earlier</b> 12:6	<b>explaining</b> 14:17
<b>counsel</b> 1:20 2:6,12 3:7 4:1 5:12 6:2 9:13 10:17,18,24 13:16 13:23 15:18 16:3 16:13 19:15	<b>december</b> 17:24 18:8 19:7,7	<b>diligence</b> 5:23	<b>effectively</b> 8:22	<b>extent</b> 15:8
<b>couple</b> 3:11 5:11 11:16	<b>decide</b> 6:7 10:13 12:23	<b>disagree</b> 7:24 13:11 15:22 16:19	<b>efficient</b> 7:11	<b>extraordinary</b> 10:22
<b>court</b> 1:1 2:12,16,22 3:2 3:9,13,17 4:1,12 4:15,18,22 5:3,4,6	<b>decided</b> 9:25 10:12 13:12		<b>effort</b> 10:16	<hr/> <b>F</b> <hr/>
	<b>deciding</b> 10:24		<b>efile</b> 19:19	<b>facilitate</b> 15:19
	<b>decision</b> 6:11 12:11 15:6		<b>efiling</b>	<b>facing</b> 5:3
				<b>fact</b> 9:3 12:22 19:1
				<b>facto</b>

18:16 <b>failure</b> 7:12,14 <b>fair</b> 10:19 <b>fairly</b> 13:1 <b>far</b> 14:11 17:14 <b>fed</b> 7:3 <b>federal</b> 6:20,25 10:5 11:12 <b>feel</b> 16:13 <b>feeling</b> 17:4 <b>figure</b> 8:15 <b>figured</b> 17:20 <b>filing</b> 19:25 <b>find</b> 2:23 6:19 16:16 <b>finding</b> 6:16 <b>fine</b> 16:9,21 18:4 <b>first</b> 3:17,19 4:5 7:15 8:20 13:10 16:7,9 17:23 <b>five</b> 13:23 16:1 18:14 <b>focus</b> 13:3 15:7,7,13 <b>follow</b> 8:7 <b>following</b> 2:10 <b>foreclosing</b> 18:20,22 <b>format</b> 14:16 16:12 <b>forward</b> 10:11,15 19:15 <b>forwarded</b>	3:23 <b>frequently</b> 9:24,24 <b>friday</b> 17:25 18:1 19:4,4 <b>front</b> 10:24 <b>fundamentally</b> 13:10 16:19 <hr/> <b>G</b> <hr/> <b>gaffigan</b> 1:24 <b>game</b> 10:19 <b>geddes</b> 1:15 2:19 <b>general</b> 3:7 <b>genome</b> 1:3 2:17,19 9:19 <b>getgo</b> 7:19 <b>getting</b> 15:3 18:15 <b>give</b> 5:11 11:16,23,24 18:14 <b>gives</b> 8:24 <b>go</b> 9:13 10:11 14:12 14:23 16:11 17:13 <b>goes</b> 6:11,21 9:5,14,20 16:8 <b>going</b> 2:22 3:18,21 4:4 4:25 9:2 10:19 13:16 15:8 16:13 18:10 19:5,21 <b>good</b> 2:12,14,18 <b>goodbye</b> 20:14 <b>gotten</b> 11:4 <b>guidance</b> 16:3	<hr/> <b>H</b> <hr/> <b>hamilton</b> 2:4 3:15 <b>hand</b> 17:13,13 <b>happened</b> 14:19 <b>happy</b> 15:17 16:2,18 20:5,6,11,13 <b>heard</b> 17:5 <b>held</b> 2:11 <b>help</b> 15:6 <b>helpful</b> 5:10 <b>highlighting</b> 12:22 <b>highly</b> 19:17,22 <b>honor</b> 2:15,18 3:4 4:8,13 4:20 5:2 8:17 11:17,22,23 13:6 13:25 14:6,8,13 14:25 15:4 16:10 16:17,25 17:8,25 18:3,10 19:12 20:1,11 <b>honorable</b> 1:12 <b>host</b> 13:20 <b>hour</b> 19:24 <b>human</b> 1:3 2:17,19 9:19 <hr/> <b>I</b> <hr/> <b>identified</b> 9:1 15:4 <b>identify</b> 3:12 4:1 <b>identifying</b> 4:9 <b>ii</b> 5:18 6:12	<b>imagine</b> 19:21 <b>immunex</b> 1:6 3:3,16 8:21 <b>important</b> 9:11 <b>indicated</b> 16:14 <b>inefficient</b> 7:16 <b>instructed</b> 5:7 <b>intend</b> 20:7 <b>interesting</b> 12:1,2 <b>interference</b> 4:17 5:18 6:9 7:9 7:11 8:25 9:19,20 9:25 10:4 <b>interrogatory</b> 10:19 <b>invention</b> 5:23 6:5 <b>inventor</b> 5:23 <b>inventors</b> 5:21 <b>inviting</b> 11:3 <b>involved</b> 9:9 <b>irrelevant</b> 9:10 10:10 13:1 <b>issue</b> 3:20,21 5:4,19,25 6:1,4,4,6,7,13,23 6:24 7:7 8:14 9:7 9:14,17 11:3 13:13,18 15:2 16:22 17:6,9,10 17:17 18:10 <b>issued</b> 6:20 8:4 <b>issues</b> 4:21,22 5:3,9,17 6:21 7:10,14,19 7:23 9:1,11,25 10:3,4,7,16,24,25	12:23 13:11,12 14:2 15:20 <hr/> <b>J</b> <hr/> <b>john</b> 1:15 2:19,22,24 <b>joseph</b> 2:4 3:14 <b>judge</b> 1:12 2:13 12:2,3,7 12:12 13:2 14:22 15:11 <b>judicial</b> 7:12,17 <b>jump</b> 10:15 <b>jurisdiction</b> 5:4 6:7 8:15,24 9:5,14,15 12:5 17:11 <b>justified</b> 18:17 <b>justify</b> 11:6 <hr/> <b>K</b> <hr/> <b>keeps</b> 19:10 <b>kenyon</b> 1:17,17 2:20,20 3:1,1 <b>kind</b> 5:8 <b>know</b> 2:16 4:23 13:2,15 13:19 15:12 16:14 17:3 <b>kwasisgroch</b> 3:6 <hr/> <b>L</b> <hr/> <b>land</b> 18:1 <b>lauren</b> 2:4 3:15 <b>law</b> 6:6,16 10:2,5 13:13,14 14:17 <b>lead</b> 10:21 11:12
--	---	---	---	--

<b>learned</b> 13:21	2:5	<b>N</b>	20:8,9	11:8,10 15:3
<b>leeway</b> 16:14	<b>lot</b> 6:10 7:20 12:2 13:4	<b>name</b> 3:19	<b>overarching</b> 6:24 7:7,22	<b>plaintiff</b> 1:4,20 16:9
<b>left</b> 5:2	<b>lower</b> 8:10	<b>names</b> 3:18	<b>P</b>	<b>plaintiffs</b> 14:22
<b>legal</b> 5:4 6:24 7:1,6,7 7:13,23,24 16:5 17:10	<b>M</b>	<b>nature</b> 5:24	<b>page</b> 12:9,10,11	<b>please</b> 2:16 3:13 20:8
<b>length</b> 16:20	<b>magistrate</b> 1:12	<b>necessarily</b> 17:12 20:7	<b>pages</b> 14:16 15:14,17,18 16:1,12,13,20,21 16:22 19:15	<b>point</b> 10:15 18:21
<b>letter</b> 10:2 13:13,22,23 14:16 16:8,12	<b>maintain</b> 18:16	<b>necessary</b> 8:12	<b>part</b> 6:15 12:14	<b>position</b> 5:20 16:6
<b>letters</b> 15:5	<b>managed</b> 6:19	<b>need</b> 4:1 6:3 16:13,15 18:5	<b>particular</b> 13:18	<b>possibly</b> 14:16
<b>level</b> 7:6,11 10:4	<b>mary</b> 1:12	<b>needs</b> 8:14	<b>parties</b> 4:20,23 7:9 12:8 12:20 16:24	<b>potential</b> 11:3
<b>levels</b> 14:3	<b>matter</b> 9:6,21 10:10 18:13	<b>never</b> 10:3,4,19	<b>party</b> 7:5,15	<b>practice</b> 5:22
<b>library</b> 15:10	<b>matters</b> 10:12	<b>new</b> 1:19,19 2:21 7:6 12:20,21,21 15:24	<b>pat</b> 1:12	<b>preclude</b> 9:9 10:17
<b>limit</b> 17:17	<b>mean</b> 13:20 18:9	<b>newman</b> 12:7,12 15:12	<b>patent</b> 4:6,10 9:25	<b>precludes</b> 9:6
<b>limited</b> 7:1 13:12 14:18 14:21 15:9	<b>meet</b> 4:20 5:8,10	<b>newmans</b> 12:2,3	<b>pen</b> 2:23	<b>preclusion</b> 8:22 11:1
<b>line</b> 2:16 3:5	<b>melanie</b> 1:22 3:4,8 4:13	<b>note</b> 2:10	<b>people</b> 3:11	<b>preclusive</b> 11:6
<b>listed</b> 16:8	<b>mention</b> 11:25	<b>notebooks</b> 5:24	<b>percent</b> 6:8	<b>present</b> 12:21
<b>listen</b> 13:17	<b>mentioned</b> 6:9,16	<b>november</b> 1:9 16:8	<b>perkins</b> 2:3 3:6,16	<b>presentation</b> 7:10,14
<b>little</b> 16:14,20 18:25	<b>merit</b> 1:25	<b>novo</b> 10:1 12:22 13:19 13:19 14:18	<b>permissive</b> 8:6	<b>presented</b> 7:1,7
<b>llp</b> 1:21	<b>michael</b> 2:3 3:5,10 4:25 5:14 14:25 15:25 16:17 17:5,16	<b>O</b>	<b>permitting</b> 7:15	<b>pretrial</b> 10:16
<b>locally</b> 2:20	<b>mind</b> 4:23 17:17	<b>office</b> 3:11 9:25 19:24	<b>perspective</b> 16:18	<b>prevents</b> 15:2
<b>lois</b> 3:6	<b>minimum</b> 6:3	<b>okay</b> 4:12 8:2 11:19 15:23 16:11 17:3 17:4 20:3	<b>pfeffer</b> 1:18 2:20,25	<b>prior</b> 10:14
<b>look</b> 8:11 12:2 19:5,15	<b>monday</b> 17:20,22,23	<b>ooo</b> 2:8	<b>phase</b> 5:18 6:10,11	<b>priority</b> 5:19 6:4,13
<b>looked</b> 13:21	<b>months</b> 6:10	<b>opposing</b> 5:12 6:2	<b>phases</b> 6:9	<b>probably</b> 13:17,22,23 15:17
<b>looking</b> 17:1	<b>motions</b> 8:8 9:9	<b>order</b> 3:23 9:6,16 10:14 10:16 15:3 18:21	<b>phone</b> 6:17	<b>problem</b> 8:3
<b>los</b>	<b>moving</b> 18:20 19:11		<b>picture</b> 6:4	<b>procedure</b> 8:7,7 13:21
			<b>place</b>	<b>proceeding</b> 7:8 12:7,20
				<b>proceedings</b> 20:9

<b>process</b> 10:17	3:18	2:20,25 4:8 8:17	19:16	19:12
<b>properly</b> 5:5 9:10 10:25 17:10	<b>refinement</b> 17:2	13:19 15:16 16:14 17:1 18:4	<b>seeking</b> 8:25 11:1	<b>stand</b> 9:4
<b>propose</b> 19:6	<b>regard</b> 5:10	<b>richard</b> 1:18	<b>separate</b> 20:7	<b>standpoint</b> 14:22
<b>proposed</b> 3:22	<b>registered</b> 1:25	<b>right</b> 3:13,17 5:13 6:14 8:7 9:18,21 10:11 11:7,10 14:14,23 15:10,19 17:13 18:3 19:2,20 20:4	<b>serve</b> 10:18	<b>stargatt</b> 1:21
<b>proposition</b> 9:12	<b>relatively</b> 14:2		<b>seven</b> 14:16 15:14,17 16:12	<b>started</b> 11:4
<b>purely</b> 16:5	<b>relevant</b> 10:24	<b>round</b> 15:24	<b>sevenpage</b> 13:23	<b>stated</b> 16:22,24
<b>pursuing</b> 10:10	<b>rely</b> 15:8	<b>rule</b> 8:20 11:2 18:15 18:18	<b>sharp</b> 1:22 3:4,4 4:13,13 4:16,19,25 20:1 20:11	<b>statement</b> 6:20
<hr/> <b>Q</b> <hr/>	<b>relying</b> 11:15	<b>rules</b> 8:6 11:12 13:21	<b>sharpen</b> 13:3	<b>states</b> 1:1 12:4
<b>question</b> 9:14 14:14 15:1 16:11	<b>remedy</b> 11:7,9	<b>ruling</b> 10:22 13:3	<b>short</b> 16:18	<b>statutory</b> 9:21
<b>quote</b> 7:2	<b>remind</b> 18:24	<hr/> <b>S</b> <hr/>	<b>show</b> 15:13	<b>stay</b> 18:16
<hr/> <b>R</b> <hr/>	<b>renders</b> 6:11	<b>safe</b> 20:13	<b>side</b> 5:21 13:25 18:24	<b>stipulate</b> 15:18
<b>raise</b> 7:15 9:18	<b>renewed</b> 12:24	<b>saying</b> 10:24 14:18	<b>sides</b> 14:10	<b>straightforward</b> 18:14
<b>raised</b> 5:17 10:3,4,8,23 13:12 16:5	<b>reporter</b> 1:25	<b>says</b> 6:25 7:2,5 10:9,19 12:18,24 15:25	<b>simply</b> 10:16	<b>subject</b> 9:2 10:1
<b>raising</b> 8:22 15:24	<b>reporters</b> 2:10	<b>schedule</b> 3:22 11:8,10 12:25	<b>simultaneous</b> 15:15	<b>submission</b> 16:12 17:18 18:7 19:4
<b>reached</b> 6:1	<b>request</b> 8:22 10:18 18:18	<b>scheduling</b> 3:23 8:21 9:6,16 10:14 15:3 18:21	<b>simultaneously</b> 16:2	<b>submissions</b> 15:15 19:16
<b>read</b> 15:10 19:5	<b>resources</b> 7:12,17,20	<b>sciences</b> 1:3	<b>sitting</b> 8:9 13:16 15:10	<b>submit</b> 18:13,18,19 19:23
<b>really</b> 15:2	<b>respect</b> 6:5	<b>scientific</b> 7:3	<b>sliger</b> 2:4 3:15	<b>successful</b> 4:24
<b>reason</b> 7:18 9:12 14:20 18:25 19:17	<b>respond</b> 2:14 18:15	<b>scientists</b> 9:19	<b>solve</b> 13:16	<b>suggest</b> 4:20
<b>reasonably</b> 10:20 11:12 12:19	<b>responds</b> 16:9	<b>scope</b> 8:1,22 9:7,22 10:13,15 13:2	<b>sorry</b> 2:22 3:9	<b>summarized</b> 15:2
<b>recognize</b> 17:19	<b>review</b> 7:8,25 8:23,25 9:2 9:7,22 10:1,13 13:19,20 14:3,12 14:18,20	<b>second</b> 6:15 17:20,22	<b>sort</b> 4:21 11:6	<b>supposed</b> 8:15
<b>record</b> 3:12 4:3 8:11 9:20 11:4 12:21	<b>reviewed</b> 8:5,8	<b>see</b> 12:10	<b>speak</b> 4:25	<b>sure</b> 16:23 18:24
<b>reduction</b> 5:22	<b>reviewing</b> 8:10	<b>seeing</b>	<b>speaker</b> 3:25	<b>suspect</b> 13:4
<b>refer</b>	<b>rich</b>		<b>speaking</b> 5:14	<hr/> <b>T</b> <hr/>
			<b>splitting</b>	<b>table</b> 9:15,16
				<b>take</b>

12:1 <b>takes</b> 6:10 <b>talking</b> 9:8 18:11 <b>taylor</b> 1:21 <b>tee</b> 15:8 <b>telephone</b> 1:10 2:10 20:15 <b>tell</b> 15:15 <b>ten</b> 6:10 16:20,21,22 <b>testimony</b> 5:24 10:7 <b>thank</b> 3:2,17 20:10,11 <b>thanksgiving</b> 17:19,20,22 19:1 19:2 20:5,6,12,13 <b>theories</b> 7:1,6,13,15,25 <b>things</b> 5:24 11:2 12:3 13:20 <b>think</b> 5:9,25 6:3,12,15 7:24 9:13 13:17 13:22 14:5,15 15:4,6,14,17,19 16:15,17,25 17:2 17:7,8,9 18:10 <b>three</b> 14:3 15:18 <b>threw</b> 17:21 19:8 <b>throw</b> 19:22 <b>thynges</b> 1:12 2:13 13:2 <b>tied</b> 10:23 <b>time</b> 5:2,18 7:16 9:11 9:18 10:15,23 18:25 19:24 <b>timing</b>	17:16 <b>today</b> 17:18 18:11,13 <b>tomorrow</b> 19:2,3 <b>transcript</b> 17:2 20:8 <b>trial</b> 7:6,16 9:3,8,10,17 10:1,11 12:22,24 <b>try</b> 4:21 5:8 15:10,19 <b>trying</b> 3:21 6:22 10:14 13:16 16:15 <b>turn</b> 5:11 11:22 13:8 <b>two</b> 6:9 8:13 14:10 18:5,12 <hr/> <b>U</b> <hr/> <b>understand</b> 4:6,18 6:14 12:4 14:7,11 15:11 17:9 <b>understanding</b> 4:5 16:23 <b>understood</b> 4:20 20:1 <b>unidentified</b> 3:25 4:3 <b>united</b> 1:1 <b>use</b> 20:8 <hr/> <b>V</b> <hr/> <b>vigorously</b> 18:16 <hr/> <b>W</b> <hr/> <b>wang</b> 11:25 <b>want</b> 7:18 15:14 16:6 16:22 17:17 18:7 <b>waste</b> 7:20 <b>wasteful</b>	7:12,17 <b>way</b> 10:22 18:19,23 <b>wednesday</b> 1:9 <b>week</b> 18:6,19,19 <b>weeks</b> 18:5,12 <b>whitmeyer</b> 9:24 <b>wilmington</b> 1:9 <b>winner</b> 11:25 <b>wise</b> 2:3 3:5,8,10,10,14 4:25 5:2,7,14,14 5:17 6:15,19 7:22 8:3,21 9:18 10:9 11:22 13:6,8,10 13:25 14:2,7,13 14:24,25 15:22 16:17,17 17:8,15 17:22,24 18:3 19:12 20:4 <b>witnesses</b> 12:21 <b>words</b> 8:23 <b>write</b> 2:24 <b>wrote</b> 3:18 <hr/> <b>X</b> <hr/> <b>Y</b> <hr/> <b>year</b> 6:21 <b>york</b> 1:19,19 2:21 <b>young</b> 1:21 3:4 <hr/> <b>Z</b> <hr/> <b>0</b> <hr/> <b>02</b> 1:9 2:11	<b>07526</b> 1:7 <hr/> <b>1</b> <hr/> <b>1</b> 1:9 2:11 20:15 <b>10</b> 19:15 <b>109</b> 11:20 <b>1098</b> 11:19,21 <b>10th</b> 19:7,7 <b>1105</b> 12:11 <b>12</b> 19:13 <b>1293</b> 7:4 <b>12th</b> 19:14 <b>1340</b> 12:1 <b>146</b> 6:16 7:8 8:24 12:5,7,20 13:11 14:3,9 <b>14th</b> 18:8 <b>198</b> 9:25 <hr/> <b>2</b> <hr/> <b>2007</b> 1:9 <b>202</b> 12:1 <b>21</b> 1:9 9:24 11:19 <b>21st</b> 17:18 18:11 <b>26</b> 8:21 <b>28</b> 20:15 <hr/> <b>3</b> <hr/> <b>35</b> 7:8 8:24	<b>3d</b> 7:4 9:24 11:19 12:1 <b>3rd</b> 17:24 19:6,7 <hr/> <b>4</b> <hr/> <b>497</b> 7:4 <hr/> <b>5</b> <hr/> <b>50</b> 6:8 <b>5th</b> 19:13,14 <hr/> <b>6</b> <hr/> <b>7</b> <hr/> <b>7th</b> 17:25 18:1,12 <hr/> <b>8</b> <hr/> <b>9</b> <hr/> <b>9th</b> 16:8
--	--	---	---	---